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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:03:25 ; Search time 61.7538 Seconds  
(without alignments)  
352.133 Million cell updates/sec

Title: US-09-114-285A-31

Perfect score: 718

Sequence: 1 MRVLILLWLFAPFGILSDV.....LARTAMDYQGQTSVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A Geneseq 19Jun03.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
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- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 718   | 100.0       | 137    | 13 AAR28671 | ppm-h1 protein pro |
| 2          | 593.5 | 82.7        | 134    | 24 ABB82796 | Antibody 806 varia |
| 3          | 588   | 81.9        | 136    | 21 AAB15672 | Murine 5B3 antibod |
| 4          | 562.5 | 78.3        | 136    | 17 AAW01144 | Mab 1.4 heavy chai |
| 5          | 562.5 | 78.3        | 136    | 19 AAW44169 | Monoclonal antibod |
| 6          | 538   | 74.9        | 138    | 13 AAR29012 | pUC-RVh-PM1f. Syn  |
| 7          | 538   | 74.9        | 138    | 13 AAR29014 | pUC-RVh-PM1f-4. S  |
| 8          | 537   | 74.8        | 260    | 21 AAY55075 | Single chain Fv pr |
| 9          | 537   | 74.8        | 367    | 21 AAY55078 | Single chain Fv pr |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 537   | 74.8 | 381 | 21 | AAY55079 | Single chain Fv pr |
| 11 | 537   | 74.8 | 519 | 21 | AAY55080 | Single chain Fv pr |
| 12 | 537   | 74.8 | 546 | 21 | AAY55074 | Single chain Fv pr |
| 13 | 537   | 74.8 | 626 | 21 | AAY55081 | Single chain Fv pr |
| 14 | 537   | 74.8 | 640 | 21 | AAY55082 | Single chain Fv pr |
| 15 | 534   | 74.4 | 119 | 18 | AAW01584 | Lead binding MAb 1 |
| 16 | 534   | 74.4 | 130 | 21 | AAY85196 | Heavy chain amino  |
| 17 | 526   | 73.3 | 130 | 14 | AAR33308 | MAE13 heavy chain. |
| 18 | 518.5 | 72.2 | 240 | 14 | AAR34510 | Fv(TU27). Homo sa  |
| 19 | 517   | 72.0 | 256 | 21 | AAY55072 | Interleukin-6 spec |
| 20 | 514   | 71.6 | 119 | 24 | AB989805 | Variable region an |
| 21 | 514   | 71.6 | 119 | 24 | AB989806 | Variable region an |
| 22 | 512.5 | 71.4 | 140 | 18 | AAW21937 | Variable heavy sub |
| 23 | 512.5 | 71.4 | 140 | 20 | AAY05267 | Antibody 24-31 hum |
| 24 | 512.5 | 71.4 | 140 | 23 | ABG98318 | Murine wild-type a |
| 25 | 510   | 71.0 | 126 | 13 | AAR24722 | Sequence encoded b |
| 26 | 505.5 | 70.4 | 225 | 15 | AAB63118 | Heavy chain of 58. |
| 27 | 501   | 69.8 | 119 | 24 | AB989808 | Variable region an |
| 28 | 500.5 | 69.7 | 114 | 15 | AAR48617 | Sequence of the mo |
| 29 | 499.5 | 69.6 | 118 | 24 | ABP58448 | Humanised antibody |
| 30 | 499.5 | 69.6 | 331 | 21 | AAY95781 | 5H7 single chain a |
| 31 | 499   | 69.5 | 213 | 16 | AAR64201 | Monoclonal antibod |
| 32 | 497.5 | 69.3 | 136 | 21 | AAY94391 | Mouse VH group I(A |
| 33 | 496   | 69.1 | 118 | 17 | AAW00829 | Variable heavy cha |
| 34 | 496   | 69.1 | 118 | 18 | AAW19015 | Anti-human FasL an |
| 35 | 495.5 | 69.0 | 121 | 11 | AAY95776 | Antibody 5H7 heavy |
| 36 | 495.5 | 69.0 | 122 | 13 | AAR24721 | Sequence of a chim |
| 37 | 493   | 68.7 | 117 | 19 | AAW39809 | Variable domain of |
| 38 | 491.5 | 68.5 | 117 | 11 | AAR07318 | VH domain of antib |
| 39 | 491.5 | 68.5 | 117 | 17 | AAW14486 | Monoclonal antibod |
| 40 | 491.5 | 68.5 | 117 | 17 | AAR99875 | Monoclonal antibod |
| 41 | 478.5 | 66.6 | 241 | 22 | AAB36827 | G28.5 svf protein. |
| 42 | 478.5 | 66.6 | 496 | 22 | AAB36828 | BD1-G28.5 fusion g |
| 43 | 476.5 | 66.4 | 118 | 24 | ABP58447 | Humanised antibody |
| 44 | 476.5 | 66.4 | 140 | 18 | AAW21935 | Variable heavy sub |
| 45 | 476.5 | 66.4 | 140 | 20 | AAY05265 | Antibody 24-31 hum |

## ALIGNMENTS

RESULT 1  
AAR28671  
ID AAR28671 standard; Protein; 137 AA.

AC AAR28671;  
XX  
DT 25-MAR-2003 (updated)  
DT 30-MAR-1993 (first entry)  
XX  
DE ppm-hi protein product.  
XX  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;  
KW plasmid; ppm-k3; ppm-h1.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..18 /note= "Signal peptide"  
FT Protein 19..137 /note= "Mature peptide"

XX WO9219759-A1.  
XX  
XX  
PD 12-NOV-1992.  
XX  
PF 24-APR-1992; 92WO-JP00544.  
XX  
PR 25-APR-1991; 91JP-0095476.  
PR 19-FEB-1992; 92JP-0032084.  
XX

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PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX
DR WPI; 1992-398882/48.
XX N-PSDB; AAQ30756.
XX
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
XX
PS Disclosure; Page 122-123; 207pp; Japanese.
XX
CC The sequences given in AAR28670-71 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognizes human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 137 AA;
Query Match 100.0%; Score 718; DB 13; Length 137;
Best Local Similarity 100.0%; Pred. No. 8.7e-58;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRVILLMLFTAFPGILSDVQLQESGVPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
DB 1 MRVILLMLFTAFPGILSDVQLQESGVPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
QY 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQTSVTVSS 137
DB 121 TTAMDYWGQTSVTVSS 137
RESULT 2
ABB82796
ID ABB82796 standard; Protein; 134 AA.
XX
AC ABB82796;
XX
DT 18-MAR-2003 (first entry)
XX
DE Antibody 806 variable heavy chain (VH) region.
XX
KW Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;
KW monoclonal antibody; mAb 806; antibody therapy; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /note= "signal peptide"
FT Protein 19..134
FT Protein /note= "mAb 806 VH region"
XX
PN WO200292771-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US15185.
XX
PR 11-MAY-2001; 2001US-290410P.
PR 28-SEP-2001; 2001US-326019P.
PR 21-DEC-2001; 2001US-342258P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX

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PI Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritter G;
PI Jungbluth A, Stockert E, Collins P, Cavenee WK, Huang H;
XX Burgess AW, Nice BC;
XX
DR WPI; 2003-129282/12.
XX N-PSDB; ABZ23940.
XX
PT Novel specific binding members, particularly antibodies recognizing
PT epidermal growth factor receptor epitope found only in tumorigenic
PT cells, useful for diagnosing, preventing and treating cancer in mammals
PT
XX
PS Claim 6; Fig 14B; 123pp; English.
XX
CC The invention relates to an isolated specific binding member (I) which
CC recognizes an epidermal growth factor receptor (EGFR) epitope which is
CC found in tumorigenic, hyperproliferative or abnormal cells and not
CC detectable in normal cells. The EGFR epitope is located within the region
CC comprising residues 273-501 of EGFR and does not demonstrate any amino
CC acid sequence alterations or substitutions from normal EGFR. (I) is
CC capable of binding the de2-7 EGFR at an epitope distinct from the
CC junctional peptide and does not bind to EGFR on normal cells in the
CC absence of aberrant expression, or in the absence of amplification of
CC normal wild-type gene. The binding member comprises the VH and VL
CC polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for
CC treating or diagnosing human or animal body, especially for treating
CC tumour in a human. (I) is useful for the preparation of a medicament and
CC for preventing or treating cancer which is located in or adjacent the
CC brain, in a mammal. (I) is also useful for detecting the presence of
CC amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation, where
CC EGFR is measured by contacting a biological sample from a mammal in which
CC the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose
CC glycosylation is suspected with (I) under conditions that allow binding
CC of the EGFR to the antibody to occur, and detecting whether binding has
CC occurred between the EGFR from the sample and the antibody, where the
CC detection of binding indicates that presence or activity of the EGFR in
CC the sample. This method is useful for detecting cancer in mammals by
CC detecting the presence or activity of an EGFR which indicates the
CC existence of a tumour or cancer in the mammal. A pharmaceutical
CC composition comprising (I), and optionally vehicle, carrier or diluent is
CC useful for preventing and/or treating cancer in mammals, especially for
CC treating brain-resident cancers that produce aberrantly expressed EGFR in
CC mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic
CC astrocytoma or neoplastic arteriovenous malformations, and malignant
CC neural tumours in mammals. The present sequence represents the mAb 806
CC VH region.
XX
SQ Sequence 134 AA;
Query Match 82.7%; Score 593.5; DB 24; Length 134;
Best Local Similarity 83.9%; Pred. No. 1.8e-46;
Matches 115; Conservative 5; Mismatches 14; Indels 3; Gaps 1;
QY 1 MRVILLMLFTAFPGILSDVQLQESGVPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
DB 1 MRVILLMLFTAFPGILSDVQLQESGVPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
QY 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQTSVTVSS 137
DB 118 GRGPPYWGQGLTVTSA 134
RESULT 3
AAB15672
ID AAB15672 standard; Protein; 136 AA.
XX
AC AAB15672;
XX
DT 08-JAN-2001 (first entry)

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XX Murine 5B3 antibody heavy chain variable region.  
 DE Mouse; 5B3 antibody; IGG1; piezoelectric immunoassay;  
 KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.  
 OS Mus sp.  
 XX WO200043774-A2.  
 PN 27-JUL-2000.  
 XX 25-JAN-2000; 2000WO-IL00048.  
 XX 25-JAN-1999; 99IL-0128212.  
 XX (YISS ) YISSUM RES & DEV CO.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX Willner I, Eshhar Z;  
 PI WPI; 2000-524259/47.  
 XX N-PSDB; AAA74604.  
 XX Apparatus for detecting small molecules, especially explosives  
 PT comprises a piezoelectric crystal -  
 XX Disclosure; Fig 3A; 90pp; English.  
 PS  
 XX The present sequence is the heavy chain variable region of 5B3 antibody.  
 CC The cDNA encoding this sequence was obtained from total RNA extracted  
 CC from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a  
 CC TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked  
 CC by very low amounts of TNT and it can therefore be used in a method for  
 CC detecting small assayed explosive molecules. Molecules are detected using  
 CC a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase  
 CC allows stationary and flow analysis of an aqueous sample. The method is  
 CC sufficiently sensitive for detection of low molecular weight molecules.  
 XX  
 SQ Sequence 136 AA;  
 Query Match 81.9%; Score 588; DB 21; Length 136;  
 Best Local Similarity 83.8%; Pred. No. 5.8e-46;  
 Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;  
 QY 1 MRVLILLWLTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFP 60  
 DB 1 MRVLILLWLTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSGYAMWNIROFP 60  
 QY 61 GNKLEWMGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTGDTSTYYCARSLAR 120  
 DB 61 GNKLEWMGYISYSGFTSNPSLSRISITRDTSKNQFFLQNLNSVTSEDTATYYCARWDYG 120  
 QY 121 TT--AMDYWGQGTSTV 134  
 DB 121 TTYGYFDVWGQGTTVT 136  
 RESULT 4  
 AAW01144  
 ID AAW01144 standard; Protein; 136 AA.  
 XX AAW01144;  
 XX 10-FEB-1997 (first entry)  
 XX MAB 1.4 heavy chain, directed against type II phospholipase A2.  
 DE Monoclonal antibody; phospholipase; myocardial infarction;  
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;  
 KW chronic rheumatism; adult respiratory distress syndrome;  
 XX cardiac shock; treatment; preclinical testing; disease; hybridoma.  
 XX

OS Mus musculus.  
 XX Key Location/Qualifiers  
 FH Binding-site 49..54  
 FT /label= CDR 1  
 FT Binding-site 69..84  
 FT /label= CDR 2  
 FT Binding-site 117..125  
 FT /label= CDR 3  
 XX  
 PN WO9620959-A1.  
 XX 11-JUL-1996.  
 PD 27-DEC-1995; 95WO-JP02714.  
 XX 29-DEC-1994; 94JP-0340006.  
 XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;  
 PI WPI; 1996-333946/33.  
 XX N-PSDB; AAT40804.  
 DR Monoclonal antibody inhibiting type II phospholipase A2 activity -  
 XX for treatment of myocardial and cerebral infarction  
 PT Claim 6; Figure 11; 69pp; Japanese.  
 PS  
 XX Monoclonal antibodies which inhibit type II phospholipase A2 are  
 CC useful in the treatment of myocardial infarction, cerebral  
 CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,  
 CC pancreatitis, adult respiratory distress syndrome and colitis. The  
 CC antibodies were generated by immunising Balb/C mice with recombinant  
 CC human type II phospholipase A2. Spleen cells from the mice were  
 CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas  
 CC obtained were screened for phospholipase A2 inhibitory activity.  
 CC Active clones were isolated including 12H5, 1.4 and 10.1. These  
 CC were cultured and the antibody isolated from the culture  
 CC supernatant by precipitation with ammonium sulphate and purification  
 CC on a column of protein A-Sepharose CL4B. Because the antibody acts  
 CC on the primate and mouse forms of enzyme as well as human it is  
 CC particularly suitable for preclinical testing.  
 XX  
 SQ Sequence 136 AA;  
 Query Match 78.3%; Score 562.5; DB 17; Length 136;  
 Best Local Similarity 81.0%; Pred. No. 1.2e-43;  
 Matches 111; Conservative 6; Mismatches 19; Indels 1; Gaps 1;  
 QY 1 MRVLILLWLTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFP 60  
 DB 1 MRVLILLWLTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFP 60  
 QY 61 GNKLEWMGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTGDTSTYYCARSLAR 120  
 DB 61 GNKLEWMGYIRYSGTYSNPSLKRISITRDTSKNQFFLHLSVTEDTATYYCTRDLD 119  
 QY 121 TTAMDYWGQGTSTVTS 137  
 DB 120 AWYFDVWGAGTIVTSS 136  
 RESULT 5  
 AAW44169  
 ID AAW44169 standard; Protein; 136 AA.  
 XX AAW44169;  
 XX 16-JUN-1998 (first entry)  
 XX Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.  
 DE

XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;  
KW amelioration; kidney disorder; nephrotoxicity; anticancer.  
XX Unidentified.  
XX WO9749427-A1.  
XX 31-DEC-1997.  
XX 27-JUN-1997; 97WO-JP02241.  
XX 19-SEP-1996; 96JP-0247635.  
XX 27-JUN-1996; 96JP-0167286.  
XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
XX Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;  
XX WPI: 1998-076914/07.  
XX N-PSDB; AAV12261.  
XX Amelioration of kidney disorders caused by cisplatin administration  
PT - by treatment with an antibody inhibiting type II phospholipase A2  
PT activity  
XX  
PS Disclosure; Page 38; 74pp; Japanese.  
XX  
CC The present sequence represents the monoclonal antibody 1.4 heavy chain  
CC against type II phospholipase A2, from the present invention. The  
CC present invention describes a novel method for the amelioration of  
CC kidney disorders (such as acute renal failure) associated with the  
CC administration of cisplatin for the treatment of cancer. The method  
CC comprises treatment with a monoclonal antibody which inhibits the  
CC activity of type II phospholipase A2 (particularly of type II  
CC phospholipase A2 of human origin), or with a protein or peptide  
CC possessing the same inhibitory activity and containing a part of the  
CC antibody sequence. Preferably the antibody also inhibits the activity of  
CC ape and/or mouse type II phospholipase A2, and has the ability to  
CC release type II phospholipase A2 bound to a cell membrane. Three  
CC specific monoclonal antibodies having these properties which can be  
CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,  
CC FERM BP-5298 and FERM BP-5297 respectively. The method can be used for  
CC suppressing the nephrotoxicity which is a characteristic feature of  
CC cisplatin administration, and therefore allowing more efficient use of  
CC this drug as an anticancer agent, e.g. by allowing an increased dosage  
CC to be used.  
XX  
SQ Sequence 136 AA;  
Query Match 78.3%; Score 562.5; DB 19; Length 136;  
Best Local Similarity 81.0%; Pred. No. 1.2e-43;  
Matches 111; Conservative 6; Mismatches 19; Indels 1; Gaps 1;  
QY 1 MRVLILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIROPP 60  
Db 1 MRVLILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIROPP 60  
QY 61 GNKLEMMGYISYGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSILAR 120  
Db 61 GNKLEMMGYISYGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSILAR 120  
QY 121 TTAMDYWGQGTSTVTVSS 137  
Db 120 AWYFDVWGAGTTVTVSS 136  
RESULT 6  
AAR29012  
ID AAR29012 standard; Protein; 138 AA.  
XX  
AC AAR29012;  
XX

DT 25-MAR-2003 (updated)  
DT 30-MAR-1993 (first entry)  
XX pUC-RVh-PW1f.  
XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;  
KW complementarity determining region; mouse; monoclonal; hybridoma;  
KW plasmid; polymerase chain reaction; amplify.  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..19  
FT /note= "Leader peptide"  
FT Region 20..49  
FT /label= FR1  
FT Region 50..55  
FT /label= CDR1  
FT Region 56..69  
FT /label= FR2  
FT Region 70..85  
FT /label= CDR2  
FT Region 86..117  
FT /label= FR3  
FT Region 118..127  
FT /label= CDR3  
FT Region 128..138  
FT /label= FR4  
XX  
XX WO9219759-A1.  
XX 12-NOV-1992.  
XX 24-APR-1992; 92WO-JP00544.  
XX 25-APR-1991; 91JP-0095476.  
XX 19-FEB-1992; 92JP-0032084.  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX Bendig MM, Jones ST, Saidanha JW, Sato K, Tsuchiya M;  
XX WPI: 1992-398882/48.  
XX N-PSDB; AAQ31360.  
XX Reconstituted human antibody to human interleukin-6 receptor -  
PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
XX  
XX Disclosure; Page 138-9; 207pp; Japanese.  
XX  
CC The sequences given in AAR29012-15 are portions of monoclonal antibodies  
CC which were encoded by plasmids derived from mouse hybridomas. The DNA  
CC encoding complementarity determining regions (CDR's) was isolated by  
CC polymerase chain reaction. These antibodies recognise human  
CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were  
CC transformed with the plasmids encoding these genes which caused the  
CC secretion of these antibodies from the hybridoma cells.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 138 AA;  
Query Match 74.9%; Score 538; DB 13; Length 138;  
Best Local Similarity 75.9%; Pred. No. 2.1e-41;  
Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;  
QY 5 ILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIROPPGNKL 64  
Db 6 ILLFVATATGVHSQVQLQESGPGVLVPSQTLTCTVTGYISITSDHAWSWIROPPGRL 65  
QY 65 EMGYISYSGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSILARTAM 124  
Db 66 EWIGVISYSGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSILARTAM 125



QY 125 DYWGQGSTVTSS 137  
 DB 126 DYWGQGSTVTSS 138

RESULT 7  
 AAR29014  
 ID AAR29014 standard; Protein; 138 AA.  
 AC AAR29014;  
 XX 25-MAR-2003 (updated)  
 DT 30-MAR-1993 (first entry)  
 XX  
 DE PUC-RVh-PM1f-4.  
 XX  
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;  
 KW complementarity determining region; mouse; monoclonal; hybridoma;  
 KW plasmid; polymerase chain reaction; amplify.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Region /note= "Leader peptide"  
 FT Region 20..49  
 FT Region /label= FR1  
 FT Region 50..55  
 FT Region /label= CDR1  
 FT Region 56..69  
 FT Region /label= FR2  
 FT Region 70..85  
 FT Region /label= CDR2  
 FT Region 86..117  
 FT Region /label= FR3  
 FT Region 118..127  
 FT Region /label= CDR3  
 FT Region 128..138  
 FT Region /label= FR4  
 XX  
 PN WO9219759-A1.  
 XX  
 PD 12-NOV-1992.  
 XX  
 PP 24-APR-1992; 92WO-JP00544.  
 XX  
 PR 25-APR-1991; 91JP-0095476.  
 PR 19-FEB-1992; 92JP-0032084.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 XX  
 DR WPI; 1992-398882/48.  
 DR N-PSDB; AAQ31365.  
 XX  
 XX Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX  
 PS Disclosure; Page 142-3; 207pp; Japanese.  
 XX  
 CC The sequences given in AAR29012-15 are portions of monoclonal antibodies  
 CC which were encoded by plasmids derived from mouse hybridomas. The DNA  
 CC encoding complementarity determining regions (CDR's) was isolated by  
 CC polymerase chain reaction. These antibodies recognise human  
 CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were  
 CC transformed with the plasmids encoding these genes which caused the  
 CC secretion of these antibodies from the hybridoma cells.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 138 AA;

Query Match 74.9%; Score 538; DB 13; Length 138;  
 Best Local Similarity 75.9%; Pred. No. 2.1e-41;  
 Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLFATPGLSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSIROPNGKL 64  
 DB 6 IILFLVATATGVHSQVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSVROPNGRL 65  
 QY 65 EWMGYISYSGITTYNPSLKRISITRTDTSKNOFFLQLSNVTTGDTSTVYCARSLARTTAM 124  
 DB 66 EWIGYISYSGITTYNPSLKRISITRTDTSKNOFFLQLSNVTTGDTSTVYCARSLARTTAM 125  
 QY 125 DYWGQGSTVTSS 137  
 DB 126 DYWGQGSTVTSS 138

RESULT 8  
 AAY55075  
 ID AAY55075 standard; Protein; 260 AA.  
 XX  
 AC AAY55075;  
 XX 25-FEB-2000 (first entry)  
 DT  
 XX  
 DE  
 XX  
 KW Single chain Fv protein sequence shPW1(deltaEAL).  
 KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
 KW antigen-binding cell; secretable functional protein; antigenic protein;  
 KW protein isolation; diagnosis; ScFv.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9960113-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PP 30-APR-1999; 99WO-JP02341.  
 XX  
 PR 20-MAY-1998; 98JP-0138652.  
 PR 01-OCT-1998; 98JP-0279876.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Tsuchiya M, Saito M, Ohtomo T;  
 XX  
 DR WPI; 2000-039382/03.  
 DR N-PSDB; AAZ40305.  
 XX  
 XX Efficient and selective isolation of a gene encoding membrane protein  
 PT with low or no antigenic binding activity, for diagnosis, study of, and  
 PT production of drugs treating abnormal functions of the protein -  
 PT  
 PS Example 7; Page 80-82; 120pp; Japanese.  
 XX  
 CC This sequence represents a single chain Fv (ScFv) sequence.  
 CC The invention relates to a method for isolating a gene encoding a  
 CC membrane-bound protein, comprising introducing a vector into a cell,  
 CC contacting an antigen with the cell expressing the fused protein encoded  
 CC by the vector on its surface to select an antigen-binding cell, and  
 CC isolating the cDNA. The vector contains DNA encoding a secretable  
 CC functional protein with antigenicity and binding affinity, and a cDNA  
 CC ligated to DNA downstream of the 3' end of the coding sequence. The  
 CC method can be used to isolate a membrane-bound protein for diagnosis and  
 CC study. It can also be used for producing drugs treating abnormal  
 CC functions of the protein. Such a technique is efficient and selective,  
 CC which is different from the prior-art transmembrane trap (TWT) method  
 CC wherein an epitope recognised by an antibody is carried in a fused  
 CC protein.  
 XX  
 SQ Sequence 260 AA;

```
Query Match          74.8%; Score 537; DB 21; Length 260;
Best Local Similarity 75.9%; Pred. No. 5.3e-41;
Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLFTAPGILSDVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKL 64
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 IILFLVATATGVDSDVQLQESGVLVRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRGL 65
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 65 EWMGYISYGITTYNPSLKSRTSITRDTSKNQFFLQLSVTTGDTSTYYCARSLARTTAM 124
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 EWIGYISYGITTYNPSLKSRTVLMRLDTSKNQFSURLSSVTAADTAVYYCARSLARTTAM 125
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 125 DYWGQTSVTSS 137
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 126 DYWGQSLVTSS 138
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
AAY5078
ID AAY5078 standard; Protein; 367 AA.
XX
AC AAY5078;
XX
DT 25-FEB-2000 (first entry)
XX
DE Single chain Fv protein sequence shPM1-Kappa.
XX
KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX
OS Synthetic.
XX
PN WO9960113-A1.
XX
PD 25-NOV-1999.
XX
PF 30-APR-1999; 99WO-JP02341.
XX
PR 20-MAY-1998; 98JP-0138652.
PR 01-OCT-1998; 98JP-0279876.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Saito M, Ohtomo T;
XX
WPI; 2000-039382/03.
DR N-PSDB; AA240308.
XX
PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein -
XX
PS Example 7; Page 86-89; 120pp; Japanese.
XX
CC This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.
XX
SQ Sequence 367 AA;

Query Match          74.8%; Score 537; DB 21; Length 367;
Best Local Similarity 75.9%; Pred. No. 8.1e-41;

QY 5 ILLWLFTAPGILSDVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKL 64
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 IILFLVATATGVDSDVQLQESGVLVRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRGL 65
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 65 EWMGYISYGITTYNPSLKSRTSITRDTSKNQFFLQLSVTTGDTSTYYCARSLARTTAM 124
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 EWIGYISYGITTYNPSLKSRTVLMRLDTSKNQFSURLSSVTAADTAVYYCARSLARTTAM 125
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 125 DYWGQTSVTSS 137
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 126 DYWGQSLVTSS 138
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
AAY5079
ID AAY5079 standard; Protein; 381 AA.
XX
AC AAY5079;
XX
DT 25-FEB-2000 (first entry)
XX
DE Single chain Fv protein sequence shPM1-MCH4.
XX
KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX
OS Synthetic.
XX
PN WO9960113-A1.
XX
PD 25-NOV-1999.
XX
PF 30-APR-1999; 99WO-JP02341.
XX
PR 20-MAY-1998; 98JP-0138652.
PR 01-OCT-1998; 98JP-0279876.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Saito M, Ohtomo T;
XX
WPI; 2000-039382/03.
DR N-PSDB; AA240309.
XX
PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein -
XX
PS Example 7; Page 90-94; 120pp; Japanese.
XX
CC This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.
XX
SQ Sequence 381 AA;

Query Match          74.8%; Score 537; DB 21; Length 381;
Best Local Similarity 75.9%; Pred. No. 8.1e-41;
```

|    | Matches | 101:  | Conservative | 15: | Mismatches | 17: | Indels | 0: | Gaps | 0: |
|----|---------|---|--------------|-----|------------|-----|--------|----|------|----|
| Qy | 5       | ILLWLFAFPGLSDVQLQESGPGVLVPKPSQSLSTCTVTGYISITSDHAWSWIRPPGNKL   | 64           | :   | :          | :   | :      | :  | :    | :  |
| Dd | 6       | IILFLVATATGVDSQVQLQESGPGVLVPKPSQSLSTCTVTGYISITSDHAWSWIRPPGNKL | 65           | :   | :          | :   | :      | :  | :    | :  |
| Qy | 65      | EWMGYISYGITTYNPSSLKRISITRRTSKNQPFQLQNSVTTGTSTYYCARSLLARTTAM   | 124          | :   | :          | :   | :      | :  | :    | :  |
| Dd | 66      | EWICYISYGITTYNPSSLKRSVTVMLRDTSKNQFSLRLSSVTAADTVVYCARSLLARTTAM | 125          | :   | :          | :   | :      | :  | :    | :  |
| Qy | 125     | DYWGQGTSTVTVSS  | 137          | :   | :          | :   | :      | :  | :    | :  |
| Dd | 126     | DYWGQGSIVTVSS   | 138          | :   | :          | :   | :      | :  | :    | :  |

|           |  |
|-----------|--|
| RESULT 11 |  |
| AAAY5080  | AAAY5080 standard; Protein; 519 AA.                                      |
| XX        |  |
| XX        | AAAY5080;  |
| XX        |  |
| DT        | 25-FEB-2000 (first entry)  |
| XX        |  |
| DE        | Single chain Fv protein sequence sHPM1(deltaEL)-BvGS3.                   |
| XX        |  |
| KW        | Gene isolation; membrane-bound protein; fusion protein; drug production; |
| KW        | antigen-binding cell; secretable functional protein; antigenic protein;  |
| KW        | protein isolation; diagnosis; ScFv.                                      |
| XX        |  |
| OS        | Synthetic.   |
| XX        |  |
| PN        | WO9960113-A1.  |
| XX        |  |
| PD        | 25-NOV-1999.   |
| XX        |  |
| PF        | 30-APR-1999; 99WO-JP02341.   |
| XX        |  |
| PR        | 20-MAY-1998; 98JP-0138652.   |
| PR        | 01-OCT-1998; 98JP-0279876.   |
| XX        |  |
| PA        | (CHUS ) CHUGAI SEIYAKU KK.   |
| XX        |  |
| PI        | Tsuchiya M, Saito M, Ohtomo T;   |
| XX        |  |
| DR        | WPI; 2000-039382/03.   |
| DR        | N-PSDB; AAZ40312.  |
| XX        |  |
| PT        | Efficient and selective isolation of a gene encoding membrane protein    |
| PT        | with low or no antigenic binding activity, for diagnosis, study of, and  |
| PT        | production of drugs treating abnormal functions of the protein -         |
| XX        |  |
| PS        | Example 7; Page 95-100; 120pp; Japanese.                                 |
| XX        |  |
| CC        | This sequence represents a single chain Fv (ScFv) sequence.              |
| CC        | The invention relates to a method for isolating a gene encoding a        |
| CC        | membrane-bound protein, comprising introducing a vector into a cell,     |
| CC        | contacting an antigen with the cell expressing the fused protein encoded |
| CC        | by the vector on its surface to select an antigen-binding cell, and      |
| CC        | isolating the cDNA. The vector contains DNA encoding a secretable        |
| CC        | functional protein with antigenicity and binding affinity, and a cDNA    |
| CC        | ligated to DNA downstream of the 3' end of the coding sequence. The      |
| CC        | method can be used to isolate a membrane-bound protein for diagnosis and |
| CC        | study. It can also be used for producing drugs treating abnormal         |
| CC        | functions of the protein. Such a technique is efficient and selective,   |
| CC        | which is different from the prior-art transmembrane trap (TMT) method    |
| CC        | wherein an epitope recognised by an antibody is carried in a fused       |
| CC        | protein.   |
| XX        |  |
| SQ        | Sequence 519 AA;   |

|           |       |  |               |
|-----------|-------|--|---------------|
| Qy        | 5     | ILLMLFAPFGIILSDVQLQESGPVLVLPKPSQSLTCTVTGYSIITSDHAWSWTRQPPGNKL            | 64            |
| Db        | 6     | IILFLVATATGDSQVQLQESGPGLVLRPSQTLSTLTCTVSGYSITSDHAWSWTRQPEGRGL            | 65            |
| Qy        | 65    | EWMGVYSYSGITTYNPSSLKSRISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAM             | 124           |
| Db        | 66    | EWIGYISYSGITTYNPSSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM            | 125           |
| Qy        | 125   | DYWGQGTSTVTVSS   | 137           |
| Db        | 126   | DYWGQGSILTVSS  | 138           |
| RESULT 12 |       |  |               |
| AA        | 55074 | standard; Protein; 546 AA.   |               |
| XX        | AC    | AA55074;   |               |
| XX        | DT    | 25-FEB-2000  | (first entry) |
| XX        | DE    | Single chain Fv protein sequence hPM1-BvGS3.                             |               |
| XX        | KW    | Gene isolation; membrane-bound protein; fusion protein; drug production; |               |
| KW        | KW    | antigen-binding cell; secretable functional protein; antigenic protein;  |               |
| KW        | KW    | protein isolation; diagnosis; ScFv.                                      |               |
| OS        | OS    | Synthetic.   |               |
| XX        | XX    | WO960113-A1.   |               |
| XX        | PN    | 25-NOV-1999.   |               |
| XX        | PD    | 30-APR-1999;   | 99WO-JP02341. |
| XX        | PF    | 20-MAY-1998;   | 98JP-0138652. |
| XX        | PR    | 01-OCT-1998;   | 98JP-0279876. |
| XX        | XX    | (CHUS ) CHUGAI SEIYAKU KK.   |               |
| XX        | PA    | Tsuchiya M, Saito M, Ohtomo T;   |               |
| XX        | PI    | WPI; 2000-039382/03.   |               |
| XX        | DR    | N-PSDB; RAZ40303.  |               |
| XX        | DR    | Efficient and selective isolation of a gene encoding membrane protein    |               |
| PT        | PT    | with low or no antigenic binding activity, for diagnosis, study of, and  |               |
| PT        | PT    | production of drugs treating abnormal functions of the protein           |               |
| XX        | XX    | Example 5; Page 73-78; 120pp; Japanese.                                  |               |
| XX        | PS    | This sequence represents a single chain Fv (ScFv) sequence.              |               |
| XX        | CC    | The invention relates to a method for isolating a gene encoding a        |               |
| CC        | CC    | membrane-bound protein, comprising introducing a vector into a cell,     |               |
| CC        | CC    | contacting an antigen with the cell expressing the fused protein encoded |               |
| CC        | CC    | by the vector on its surface to select an antigen-binding cell, and      |               |
| CC        | CC    | isolating the cDNA. The vector contains DNA encoding a secretable        |               |
| CC        | CC    | functional protein with antigenicity and binding affinity, and a cDNA    |               |
| CC        | CC    | ligated to DNA downstream of the 3' end of the coding sequence. The      |               |
| CC        | CC    | method can be used to isolate a membrane-bound protein for diagnosis and |               |
| CC        | CC    | study. It can also be used for producing drugs treating abnormal         |               |
| CC        | CC    | functions of the protein. Such a technique is efficient and selective,   |               |
| CC        | CC    | which is different from the prior-art transmembrane trap (TMT) method    |               |
| CC        | CC    | wherein an epitope recognised by an antibody is carried in a fused       |               |
| CC        | CC    | protein.   |               |
| XX        | XX    | Sequence   | 546 AA;       |
| SQ        |       |  |               |

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRPPGNKL 64  
 Db 6 IILFLVATATGVDVQVQLQESGPGVLRPSQTLSLCTVSGYISITSDHAWSWVRQPPGRGL 65  
 QY 65 EWMGYISYSGITTYNPSLKSRISTRDTSKNOFFLQNLNSVTTGDTSTYYCARSARTTAM 124  
 Db 66 EWIGYISYSGITTYNPSLKSRISTRDTSKNOFFLQNLNSVTTGDTSTYYCARSARTTAM 125  
 QY 125 DYWGOGTSVTVSS 137  
 Db 126 DYWGQGS�VTVSS 138

## RESULT 13

AY55081  
 ID AAY55081 standard; Protein; 626 AA.

XX AC AAY55081;

XX DT 25-FEB-2000 (first entry)

XX DE Single chain Fv protein sequence sHPM1-kappa-BvGS3.

XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
 KW antigen-binding cell; secreted functional protein; antigenic protein;  
 KW protein isolation; diagnosis; ScFv.

XX OS Synthetic.

XX PN WO9960113-A1.

XX PD 25-NOV-1999.

XX PF 30-APR-1999; 99WO-JP02341.

XX PR 20-MAY-1998; 98JP-0138652.

XX PR 01-OCT-1998; 98JP-0279876.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240316.

XX PT Efficient and selective isolation of a gene encoding membrane protein  
 PT with low or no antigenic binding activity, for diagnosis, study of, and  
 PT production of drugs treating abnormal functions of the protein -

XX PS Example 7; Page 103-109; 120pp; Japanese.

XX CC This sequence represents a single chain Fv (ScFv) sequence.

XX CC The invention relates to a method for isolating a gene encoding a  
 CC membrane-bound protein, comprising introducing a vector into a cell,  
 CC contacting an antigen with the cell expressing the fused protein encoded  
 CC by the vector on its surface to select an antigen-binding cell, and  
 CC isolating the cDNA. The vector contains DNA encoding a secreted  
 CC functional protein with antigenicity and binding affinity, and a cDNA  
 CC ligated to DNA downstream of the 3' end of the coding sequence. The  
 CC method can be used to isolate a membrane-bound protein for diagnosis and  
 CC study. It can also be used for producing drugs treating abnormal  
 CC functions of the protein. Such a technique is efficient and selective,  
 CC which is different from the prior-art transmembrane trap (TWT) method  
 CC wherein an epitope recognised by an antibody is carried in a fused  
 CC protein.

XX SQ Sequence 626 AA;

Query Match 74.8%; Score 537; DB 21; Length 626;

Best Local Similarity 75.9%; Pred. No. 1.4e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRPPGNKL 64

Db 6 IILFLVATATGVDVQVQLQESGPGVLRPSQTLSLCTVSGYISITSDHAWSWVRQPPGRGL 65  
 QY 65 EWMGYISYSGITTYNPSLKSRISTRDTSKNOFFLQNLNSVTTGDTSTYYCARSARTTAM 124  
 Db 66 EWIGYISYSGITTYNPSLKSRISTRDTSKNOFFLQNLNSVTTGDTSTYYCARSARTTAM 125  
 QY 125 DYWGOGTSVTVSS 137  
 Db 126 DYWGQGS�VTVSS 138

## RESULT 14

AY55082

ID AAY55082 standard; Protein; 640 AA.

XX AC AAY55082;

XX DT 25-FEB-2000 (first entry)

XX DE Single chain Fv protein sequence sHPM1-MCH4-BvGS3.

XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
 KW antigen-binding cell; secreted functional protein; antigenic protein;  
 KW protein isolation; diagnosis; ScFv.

XX OS Synthetic.

XX PN WO9960113-A1.

XX PD 25-NOV-1999.

XX PF 30-APR-1999; 99WO-JP02341.

XX PR 20-MAY-1998; 98JP-0138652.

XX PR 01-OCT-1998; 98JP-0279876.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240321.

XX PT Efficient and selective isolation of a gene encoding membrane protein  
 PT with low or no antigenic binding activity, for diagnosis, study of, and  
 PT production of drugs treating abnormal functions of the protein -

XX PS Example 7; Page 111-117; 120pp; Japanese.

XX CC This sequence represents a single chain Fv (ScFv) sequence.

XX CC The invention relates to a method for isolating a gene encoding a  
 CC membrane-bound protein, comprising introducing a vector into a cell,  
 CC contacting an antigen with the cell expressing the fused protein encoded  
 CC by the vector on its surface to select an antigen-binding cell, and  
 CC isolating the cDNA. The vector contains DNA encoding a secreted  
 CC functional protein with antigenicity and binding affinity, and a cDNA  
 CC ligated to DNA downstream of the 3' end of the coding sequence. The  
 CC method can be used to isolate a membrane-bound protein for diagnosis and  
 CC study. It can also be used for producing drugs treating abnormal  
 CC functions of the protein. Such a technique is efficient and selective,  
 CC which is different from the prior-art transmembrane trap (TWT) method  
 CC wherein an epitope recognised by an antibody is carried in a fused  
 CC protein.

XX SQ Sequence 640 AA;

Query Match 74.8%; Score 537; DB 21; Length 640;

Best Local Similarity 75.9%; Pred. No. 1.4e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRPPGNKL 64

Db 6 IILFLVATATGVDQVQLQESGPGGLVLRPSQTLSTCTVGVSIITSDHAWSVWRPPGRGL 65  
Qy 65 EWMGYISYGITTYNPSLKSRISITRDTSKNQFFLQLNSVTGTSTYYCARSILARTTAM 124  
Db 66 EWIGYISYGITTYNPSLKSRVTMLRDTSKNQFSLRSSVTAADTAVYCARSLARTTAM 125  
Qy 125 DYWGQGTSTVTSS 137  
Db 126 DYWGQGLVTVSS 138

## RESULT 15

AAW01584  
ID AAW01584 standard; Protein; 119 AA.

XX AC AAW01584;

DT 22-AUG-1997 (first entry)

DE Lead binding MAB 13D10 heavy chain variable region.

XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
KW heavy metal.

XX OS Mus musculus.

XX PN W09639518-A1.

XX FD 12-DEC-1996.

XX XX 05-JUN-1996; 96WO-US09258.

XX XX 10-OCT-1995; 95US-0541373.

PR 05-JUN-1995; 95US-0462798.

XX PA (BION-) BIONEERASKA INC.

XX PI Lopez O, Murray PJ, Wylie DE;

XX DR WPI; 1997-043140/04.

DR N-FSDB; AAT58258.

XX DNA encoding heavy metal binding polypeptide sequences - used for  
PT detecting, removing, adding or neutralising heavy metals, such as  
PT lead cations

XX PS Claim 12; Page 71; 125pp; English.

XX The present sequence represents the heavy chain variable region for  
CC monoclonal antibody (Mab) 13D10, which immunoreacts with a lead cation.  
CC The sequence was derived from RNA isolated from mouse hybridoma cells.  
CC The protein can be used for binding heavy metals, such as lead cations.  
CC It can be used for detecting, removing, adding or neutralising the  
CC heavy metals in biological and inanimate systems. It can be used in  
CC e.g. aqueous liquid systems, in biological or environmental systems or  
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health  
CC care products, skin treatment products, pesticides, herbicides,  
CC solvents used in the production of semi-conductor and integrated  
CC circuit components and production materials for electronic components.  
CC The products can provide for applications involving minute amounts of  
CC specific heavy metals.

XX SQ Sequence 119 AA;

Query Match 74.4%; Score 534; DB 18; Length 119;

Best Local Similarity 85.7%; Pred. No. 4.1e-41;

Matches 102; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 19 DVQLQESGPGVLVKPSQSLSLTCTVGTSGYISITSDHAWSVWRPPGNKLEWGYISYGITY 78

Db 1 DVQLQESGPGVLVKPSQSLSLTCTVGTSGYISITSDHAWSVWRPPGNKLEWGYISYGITY 60

Qy 79 NPSLKSRISITRDTSKNQFFLQLNSVTGTSTYYCARSILARTTAMDYWGQGTSTVTSS 137  
Db 61 NPSLKSRISITRDTSKNQFFLQLNSVTGTSTYYCARSILARTTAMDYWGQGTSTVTSS 119

Search completed: October 22, 2003, 22:16:37  
Job time : 63.7538 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:50 ; Search time 25.947 Seconds  
(without alignments)  
507.771 Million cell updates/sec

Title: US-09-114-285A-31  
Perfect score: 718  
Sequence: 1 MRVLILLWLFAPFGILSDV.....LARTAMDYWGQTSVTSS 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*  
1: Pirl1.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 603.5 | 84.1        | 135    | 2  | PL0100      |
| 2          | 593   | 82.6        | 149    | 2  | S30752      |
| 3          | 585.5 | 78.8        | 134    | 2  | S24672      |
| 4          | 543   | 75.6        | 116    | 1  | HVMS1B      |
| 5          | 538   | 74.9        | 137    | 1  | AVMS35      |
| 6          | 536   | 74.7        | 119    | 2  | C53285      |
| 7          | 532   | 74.1        | 117    | 2  | I28195      |
| 8          | 520.5 | 72.5        | 116    | 2  | S38718      |
| 9          | 519.5 | 72.4        | 136    | 2  | S07637      |
| 10         | 517.5 | 72.1        | 114    | 2  | T01262      |
| 11         | 510   | 71.0        | 116    | 1  | HVMS31      |
| 12         | 486   | 67.7        | 121    | 2  | S37200      |
| 13         | 479   | 66.7        | 119    | 2  | E25114      |
| 14         | 478.5 | 66.6        | 106    | 2  | S26464      |
| 15         | 477.5 | 66.5        | 115    | 2  | D33932      |
| 16         | 476   | 66.3        | 117    | 2  | I57810      |
| 17         | 474   | 66.0        | 119    | 2  | C25114      |
| 18         | 467   | 65.0        | 106    | 2  | S59639      |
| 19         | 466.5 | 65.0        | 120    | 2  | A25114      |
| 20         | 461.5 | 64.3        | 117    | 1  | HVMS73      |
| 21         | 455   | 63.4        | 123    | 2  | S42771      |
| 22         | 453   | 63.1        | 115    | 2  | F25114      |
| 23         | 450   | 62.7        | 113    | 1  | G2MS60      |
| 24         | 445   | 62.0        | 119    | 2  | D25114      |
| 25         | 433.5 | 60.4        | 104    | 2  | S26467      |
| 26         | 423   | 58.9        | 140    | 2  | I37782      |
| 27         | 419.5 | 58.4        | 100    | 2  | S14485      |
| 28         | 416.5 | 58.0        | 102    | 2  | S14488      |
| 29         | 414.5 | 57.7        | 101    | 2  | S14484      |

30 414.5 57.7 155 2 S31511 Ig heavy chain - h  
31 412.5 57.5 155 2 S31512 Ig heavy chain - h  
32 408 56.8 147 2 S31519 Ig heavy chain v r  
33 407 56.7 130 2 S31690 Ig heavy chain v r  
34 406.5 56.6 102 2 S14486 Ig heavy chain v r  
35 405 56.4 146 2 S09711 Ig heavy chain v r  
36 404.5 56.3 137 2 S31676 Ig heavy chain v r  
37 402 56.0 102 2 S14487 Ig heavy chain v r  
38 399.5 55.6 141 2 S54236 Ig mu heavy chain  
39 395.5 55.1 145 2 S78055 Ig heavy chain pre  
40 394.5 54.9 139 2 S31586 Ig heavy chain v r  
41 394 54.9 123 2 S30530 Ig heavy chain v r  
42 394 54.9 135 2 S78051 Ig heavy chain pre  
43 394 54.9 139 2 A32456 Ig heavy chain pre  
44 391.5 54.5 143 2 S54249 Ig mu heavy chain  
45 391 54.5 112 2 S13685 Ig heavy chain v r

## ALIGNMENTS

### RESULT 1

PL0100  
Ig heavy chain precursor V region (40-140) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 23-Jul-1999  
C;Accession: PL0100  
R;Near: R.I.; Haber, E.  
Mol. Immunol. 26, 371-382, 1989  
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge  
A;Reference number: PL0100; MUID:89238344; PMID:2497340  
A;Accession: PL0100  
A;Molecule type: DNA  
A;Residues: 1-135 <NEA>  
A;Cross-references: GB:M27660; NID:G341745; PIDN:AAA58746.1; PID:G609530  
A;Experimental source: strain A/J  
A;Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family  
C;Genetics:  
A;Introns: 15/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-115/Domain: V segment #status predicted <VRE>  
F;33-116/Domain: immunoglobulin homology <IMV>  
F;117-118/Domain: D segment #status predicted <DRE>  
F;119-135/Domain: J segment #status predicted <JRE>

Query Match 84.1%; Score 603.5; DB 2; Length 135;  
Best Local Similarity 84.7%; Pred. No. 9.9e-46;  
Matches 116; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MRVLILLWLFAPFGILSDVQLQESGVLKPSQSLTCTVTCYTSQHWMSIRQFP 60  
Db 1 MRVLILLWLFAPFGILSDVQLQESGVLKPSQSLTCTVTCYTSQHWMSIRQFP 60  
Qy 61 GNKLEWNGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTGDTSTYYCARSLAR 120  
Db 61 GNKLEWNGYITNGYTYNPSLKRISITRDTSKNQFLQLSSVTEDTATYYCARSY-- 118

Qy 121 TTAMDYWGQTSVTSS 137  
Db 119 -DYFDYWGQTTLTSS 134

### RESULT 2

S30752  
Ig heavy chain precursor V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 23-Jul-1999  
C;Accession: S30752  
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.  
Nucleic Acids Res. 15, 5496, 1987  
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

A:Reference number: S30751; MUID:87260030; PMID:3601683

A:Accession: S30752

A:Molecule type: mRNA

A:Residues: 1-149 <GRA>

C:Cross-references: EMBL:X05878; NID:G52526; PIDN:CAA29302.1; PID:G52527

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-116/Domain: immunoglobulin homology <IMM>

F:138-149/Domain: C region (C-gamma 2b) (fragment) #status predicted <CRE>

Query Match

Best Local Similarity 82.6%; Score 593; DB 2; Length 149;

Matches 116; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

```
QY 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGYSITSDHAWSIROFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGYSITSGYTHWIRQFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 GNKLEWMGYISGITYNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 GNKLEWMGYIHSGTDFNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 121 TTAMDYWGQGTSTVTVSS 137
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 YVAMDYWGQGTSTVTVSS 137
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

RESULT 3

B24672

Ig heavy chain precursor V region (VGAM3-2) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 18-Oct-1996

C:Accession: B24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: B24672

A:Molecule type: DNA

A:Residues: 1-134 <WIN>

A>Note: This sequence was determined from the differentiated gene

C:Genetics:

A:Insertions: 15/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.8%; Score 565.5; DB 2; Length 134;

Matches 113; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

```
QY 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGYSITSDHAWSIROFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGIFITSGYSHWIRQFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
QY 61 GNKLEWMGYISGITYNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 GNKLEWMGYIHSGTDFNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCARYY-- 118
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

QY 121 TTAMDYWGQGTSTVTVSS 137

Db 119 -DYFAYWGQGLTVTSA 134

RESULT 4

HVMS1B

Ig heavy chain precursor V region (IB43) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Aug-1996

C:Accession: J0508

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J0501; MUID:89279149; PMID:2499654

A:Accession: J0508

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-116 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: this sequence belongs to the VH3660 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-116/Product: Ig heavy chain V region (IB43) #status predicted <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 543; DB 1; Length 116;

Best Local Similarity 90.5%; Pred. No. 1.6e-40;

Matches 105; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```
QY 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGYSITSDHAWSIROFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MRVILLMLFTAPFGILSDVQLQESGPDVLPKPSQSLTCTVTGYSITSGYSHWIRQFP 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
QY 61 GNKLEWMGYISGITYNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 GNKLEWMGYIHSGTDFNPSPKSRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

RESULT 5

AVMS35

Ig heavy chain precursor V region (MOPC 315) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 24-Apr-1984 #sequence\_revision 30-Jun-1992 #text\_change 22-Jun-1999

C:Accession: PL0102; S03262; A93814; A91462; A93787; S235599

R:Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.

Mol. Immunol. 26, 431-434, 1989

A:Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.

A:Reference number: PL0102; MUID:89238351; PMID:2497341

A:Accession: PL0102

A:Molecule type: mRNA

A:Residues: 1-137 <RIN>

A:Cross-references: GB:M27638; NID:G602706; PIDN:AAA61337.1; PID:G602707

A:Experimental source: strain MOPC 315

R:Rinfret, A.; Dorrington, K.J.; Klein, M.

submitted to the EMBL Data Library, June 1988

A:Reference number: S03262

A:Accession: S03262

A:Molecule type: DNA

A:Residues: 1-15,'G',16-137 <RI2>

A:Cross-references: EMBL:X07880; NID:G51760; PIDN:CAA30727.1; PID:G295908

R:Jilka, R.L.; Pestka, S.

Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977

A:Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he

A:Reference number: A93814; MUID:78094475; PMID:414225

A:Accession: A93814

A:Molecule type: protein

A:Residues: 1-14,'H',16-31 <JIL>

A>Note: the authors translated mRNA in vitro to obtain the precursor protein

R:Schlechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.

Fed. Proc. 38, 1839-1845, 1979

A:Title: Structure and function of immunoglobulin genes and precursors.

A:Reference number: A91462; MUID:79148758; PMID:428562

A:Accession: A91462

A:Molecule type: protein

A:Residues: 1,'X',3-11,'X',14-21 <SCH>

A>Note: the authors translated mRNA in vitro to obtain the precursor protein

R:Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.

Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974

A:Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse

A:Reference number: A93787; MUID:74170779; PMID:4524622

A:Accession: A93787

A:Molecule type: protein

A:Residues: 19-52,'K',53-75,'BYGB',80-101,'D',103-106,'ZB',109-122,124-137 <FRA>

R:Hood, L.; Margolies, M.; Givol, D.; Zakut, R.

unpublished results, cited by Padian, E.A., Davies, D.R., Pecht, I., Givol, D., and Wrig



C/Species: Mus musculus (house mouse)  
C/Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
C/Accession: I28195  
J./Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A/Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid sequence  
A/Reference number: A28195; MUID:88153717; PMID:3267217  
A/Accession: I28195  
A/Molecule type: mRNA  
A/Residues: 1-117 <SHE>  
A/Cross-references: GB:MI9775; NID:G195526; PIDN:AAA38343.1; PID:G195527  
A/Note: the authors translated the codon AAC for residue 61 as Thr, and did not translate  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 532; DB 2; Length 117;  
Best Local Similarity 85.7%; Pred. No. 1.4e-39;  
Matches 102; Conservative 67; Mismatches 9; Indels 2; Gaps 1;

Qy 19 DVLOQESGPIVLKPSQSLTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYSGITTY 78  
Db 1 DVLOQESGPIVLKPSQSLTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYSGITTY 60

Qy 79 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137  
Db 61 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARD--NGNCGDYWGQGTSTVTVSS 117

RESULT 8  
S38718  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S38718  
F/Cimanis, A.Y.  
submitted to the EMBL Data Library, November 1993  
A/Reference number: S38713  
A/Accession: S38718  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-116 <CIM>  
A/Cross-references: EMBL:X76018; NID:G416102; PIDN:CAA53605.1; PID:G1334263  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 520.5; DB 2; Length 116;  
Best Local Similarity 84.0%; Pred. No. 1.4e-38;  
Matches 100; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

Qy 19 DVLOQESGPIVLKPSQSLTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYSGITTY 78  
Db 1 DVLOQESGPIVLKPSQSLTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYSGITTY 60

Qy 79 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137  
Db 61 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARG--GTGFTFWGQGTLTIVSA 116

RESULT 9  
S07637  
Ig heavy chain V region (PTF.02) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 23-Jul-1999  
C/Accession: S07637  
R./Urakov, D.N.; Deev, S.M.; Polyakovskiy, O.L.  
Nucleic Acids Res. 17, 9481, 1989  
A/Title: The structure of the expressible VH gene from a hybridoma producing monoclonal  
A/Reference number: S07637; MUID:90067954; PMID:2587273  
A/Accession: S07637  
A/Molecule type: DNA  
A/Residues: 1-136 <URA>

A;Cross-references: EMBL:X16740; NID:G52099; PIDN:CAA34714.1; PID:G297543  
A;Note: the authors translated the codon TAT for residue 112 as Ile, TAC for residue 113  
C;Genetics: 15/3  
A;introns: 15/3  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 519.5; DB 2; Length 136;  
Best Local Similarity 72.7%; Pred. No. 2.1e-38;  
Matches 104; Conservative 9; Mismatches 17; Indels 13; Gaps 2;  
  
QY 1 MRVILLWLFTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFP 60  
DB 1 MKVLSLLYLLTAIPGILSTVQLQESGVLVVKPSQSLTCTVTGYSITSGYYWHWIROFP 60  
  
QY 61 GNKLEWGMGYSISGITYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120  
DB 61 GNKLEWGMGYSIDGNGYNPSLKRISITRDTSKNQFFLQNSVTTEDTATYYCTRG--- 117  
  
QY 121 TTAMD-----YWGQGSTVTVSS 137  
DB 118 ----DCYHFFTYWGQGLTVTSA 136

RESULT 10  
T01262  
Ig heavy chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 21-Jul-2000  
C;Accession: T01262  
R;Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.  
AIDS Res. Hum. Retroviruses 9, 41-49, 1993  
A;Title: Variable region gene utilization and mutation in a group of neutralizing murine  
A;Reference number: Z14285; MUID:93152285; PMID:7678971  
A;Accession: T01262  
A;Status: preliminary;  
A;Molecule type: mRNA  
A;Residues: 1-114 <PIR>  
A;Cross-references: EMBL:S54194; NID:G264864; PIDN:AAB25246.2; PID:G5705887  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 517.5; DB 2; Length 114;  
Best Local Similarity 83.2%; Pred. No. 2.6e-38;  
Matches 99; Conservative 8; Mismatches 7; Indels 5; Gaps 1;  
  
QY 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFPGNKLEWGMGYSISGITY 78  
DB 1 DVQLQESGVLVVKPSQSLTCTVTGYSITSDYANNWIRQFPGNKLEWGMGYSISGITY 60  
  
QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTAMDYWGQGSTVTVSS 137  
DB 61 NPSLKRISITRDTSKNLFQNSVTTEDTATYYCARGLP-----DYWGQGSTVTVSS 114

RESULT 11  
HWS31  
Ig heavy chain precursor V region (M315) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Aug-1996  
C;Accession: JT0509  
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A;Reference number: JT0501; MUID:89279149; PMID:2499654  
A;Accession: JT0509  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-116 <LEV>  
A;Experimental source: strain BALB/cJ  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-116/Product: Ig heavy chain V region (M315) #status predicted <MAT>  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 510; DB 1; Length 116;  
Best Local Similarity 83.6%; Pred. No. 1.2e-37;  
Matches 97; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MRVILLWLFTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFP 60  
DB 1 MKVLSLLYLLTAIPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSGYYWHWIROFP 60  
  
QY 61 GNKLEWGMGYSISGITYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116  
DB 61 GNKLEWGMGYSIDGNGYNPSLKRISITRDTSKNQFFLQNSVTTEDTATYYCAR 116

RESULT 12  
S37200  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
C;Accession: S37200  
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
submitted to the EMBL Data Library, August 1993  
A;Description: Production and cloning of TMV-specific monoclonal antibodies.  
A;Reference number: S37200  
A;Accession: S37200  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-121 <FTS>  
A;Cross-references: EMBL:X74587; NID:G402639; PID:G402640  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 486; DB 2; Length 121;  
Best Local Similarity 77.7%; Pred. No. 1.5e-35;  
Matches 94; Conservative 8; Mismatches 17; Indels 2; Gaps 1;  
  
QY 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIROFPGNKLEWGMGYSISGITY 78  
DB 1 DVQLQESGVLVVKPSQSLTCTVTGYSITSSYYNNWIRQFPGNKLEWGMGYSISGITY 60  
  
QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTAMDYWGQGSTVTVSS 136  
DB 61 NPSLKRISITRDTSKNQFFLQNSVTTEDTATYYCARGGIYGYDDYFDSWGQGSTVTVSS 120  
  
QY 137 S 137  
DB 121 S 121

RESULT 13  
E25114  
Ig heavy chain V region (HP25) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
C;Accession: E25114  
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
EMBO J. 4, 3681-3688, 1985  
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin  
A;Reference number: A91028; MUID:86136012; PMID:3937730  
A;Accession: E25114  
A;Molecule type: mRNA  
A;Residues: 1-119 <OLL>  
A;Cross-references: GB:X03378; NID:G52007; PIDN:CAA27095.1; PID:g1334016  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 479; DB 2; Length 119;  
Best Local Similarity 78.2%; Pred. No. 6.1e-35;  
Matches 93; Conservative 6; Mismatches 14; Indels 6; Gaps 1;

|    |    |                              |                             |                             |     |
|----|----|------------------------------|-----------------------------|-----------------------------|-----|
| Qy | 61 | GNKLEWGYISYSGIITTYNPSLKSRSIS | TRDTSKNQFFLQINSVTGDTSTYYCAR | 116                         |     |
|    |    | :                            | :                           |                             |     |
|    |    | :                            | :                           |                             |     |
| Db | 60 | GNKLEWGYISYSGSTYVNP          | SLKSRSIS                    | TRDTSKNQYVLOINSVTEDTATYYCAR | 115 |
|    |    | :                            | :                           |                             |     |
|    |    | :                            | :                           |                             |     |

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:20 ; Search time 14.0114 Seconds  
(without alignments)  
459.817 Million cell updates/sec

Title: US-09-114-285a-31

Perfect score: 718

Sequence: 1 MRVLLWLFTAFPGILSDV.....LARTAMDYWGQTSVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 543   | 75.6        | 116    | 1 HV61_MOUSE | P18532 mus musculu |
| 2          | 538   | 74.9        | 137    | 1 HV46_MOUSE | P01822 mus musculu |
| 3          | 510   | 71.0        | 116    | 1 HV60_MOUSE | P18531 mus musculu |
| 4          | 461.5 | 64.3        | 117    | 1 HV62_MOUSE | P18533 mus musculu |
| 5          | 450   | 62.7        | 113    | 1 HV47_MOUSE | P01823 mus musculu |
| 6          | 384.5 | 53.6        | 144    | 1 HV43_MOUSE | P01819 mus musculu |
| 7          | 377.5 | 52.6        | 146    | 1 HV21_HUMAN | P06331 homo sapien |
| 8          | 338   | 47.1        | 135    | 1 HV02_XENLA | P20957 xenopus lae |
| 9          | 337   | 46.9        | 117    | 1 HV2G_HUMAN | P01825 homo sapien |
| 10         | 330   | 46.0        | 115    | 1 HV44_MOUSE | P01820 mus musculu |
| 11         | 328   | 45.7        | 129    | 1 HV2F_HUMAN | P01824 homo sapien |
| 12         | 323   | 45.0        | 121    | 1 HV2E_HUMAN | P01818 homo sapien |
| 13         | 316   | 44.0        | 116    | 1 HV45_MOUSE | P01821 mus musculu |
| 14         | 312.5 | 43.5        | 136    | 1 HV01_XENLA | P20956 xenopus lae |
| 15         | 308   | 42.9        | 119    | 1 HV2C_HUMAN | P01816 homo sapien |
| 16         | 295.5 | 41.2        | 147    | 1 HV2H_HUMAN | P04438 homo sapien |
| 17         | 295   | 41.1        | 125    | 1 HV2D_HUMAN | P01817 homo sapien |
| 18         | 291.5 | 40.6        | 120    | 1 HV2B_HUMAN | P01815 homo sapien |
| 19         | 289.5 | 40.3        | 136    | 1 HV16_MOUSE | P01783 mus musculu |
| 20         | 287.5 | 40.0        | 139    | 1 HV07_MOUSE | P01751 mus musculu |
| 21         | 287   | 40.0        | 140    | 1 HV02_MOUSE | P01746 mus musculu |
| 22         | 285.5 | 39.8        | 137    | 1 HV11_MOUSE | P01755 mus musculu |
| 23         | 280   | 39.0        | 115    | 1 HV3F_HUMAN | P01767 homo sapien |
| 24         | 278.5 | 38.8        | 122    | 1 HV3H_HUMAN | P01769 homo sapien |
| 25         | 277.5 | 38.6        | 126    | 1 HV3A_HUMAN | P01814 homo sapien |
| 26         | 277   | 38.6        | 119    | 1 HV3G_HUMAN | P01773 homo sapien |
| 27         | 276.5 | 38.5        | 122    | 1 HV3J_HUMAN | P01768 homo sapien |
| 28         | 276   | 38.4        | 117    | 1 HV13_MOUSE | P01757 mus musculu |
| 29         | 274   | 38.2        | 117    | 1 HV17_MOUSE | P01786 mus musculu |
| 30         | 274   | 38.2        | 136    | 1 HV15_MOUSE | P01759 mus musculu |
| 31         | 273   | 38.0        | 120    | 1 HV03_MOUSE | P01747 mus musculu |
| 32         | 272   | 37.9        | 117    | 1 HV42_MOUSE | P01812 mus musculu |
| 33         | 272   | 37.9        | 121    | 1 HV3J_HUMAN | P01771 homo sapien |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 34 | 272   | 37.9 | 142 | 1 HV01_RAT   | P01805 rattus norv |
| 35 | 271   | 37.7 | 117 | 1 HV12_MOUSE | P01756 mus musculu |
| 36 | 266.5 | 37.1 | 122 | 1 HV3A_HUMAN | P01762 homo sapien |
| 37 | 266.5 | 37.1 | 126 | 1 HV3K_HUMAN | P01772 homo sapien |
| 38 | 265.5 | 37.0 | 119 | 1 HV40_MOUSE | P01810 mus musculu |
| 39 | 265   | 36.9 | 117 | 1 HV14_MOUSE | P01758 mus musculu |
| 40 | 264.5 | 36.8 | 116 | 1 HV3T_HUMAN | P01781 homo sapien |
| 41 | 264.5 | 36.8 | 118 | 1 HV51_MOUSE | P06330 mus musculu |
| 42 | 264.5 | 36.8 | 119 | 1 HV38_MOUSE | P01808 mus musculu |
| 43 | 262   | 36.5 | 117 | 1 HV3C_HUMAN | P01764 homo sapien |
| 44 | 262   | 36.5 | 117 | 1 HV41_MOUSE | P01811 mus musculu |
| 45 | 262   | 36.5 | 117 | 1 HV54_MOUSE | P18525 mus musculu |

ALIGNMENTS

RESULT 1  
HV61\_MOUSE STANDARD; PRT; 116 AA.  
AC P18532;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 1B43 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;  
RX MEDLINE=89279149; PubMed=2499654;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
the primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.  
DR PIR; JTO508; HVMS1B.  
DR PDB; 1KCS; 11-MAY-02.  
DR PDB; 1KCV; 11-MAY-02.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.  
FT SIGNAL 1 18  
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.  
FT DOMAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 54 67 FRAMEWORK-2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 85 116 FRAMEWORK-3.  
FT DISULFID 40 114 BY SIMILARITY.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 75.6%; Score 543; DB 1; Length 116;  
Best Local Similarity 90.5%; Pred. No. 7e-46;  
Matches 105; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

|    |    |  |     |
|----|----|--|-----|
| Qy | 1  | MRVLLWLFTAFPGILSDVQLQESGVLKPKSLSLTCTVTCTGYSITSDHAWSIROFP | 60  |
| Db | 1  | MRVLLWLFTAFPGILSDVQLQESGVLKPKSLSLTCTVTCTGYSITSDHAWSIROFP | 60  |
| Qy | 61 | GNKLEWNGYISYSGITTYNPNLSKRSITRDTSKNQFFLQNSVTTGDTSTYYCAR   | 116 |
| Db | 61 | GNKLEWNGYIHYSGNTSYNPNLSKRSITRDTSKNQFFLQNSVTTGDTSTYYCAR   | 116 |

RESULT 2



```
QY 1 MRVLLILLWLTAFPGILSDVOLQBSGPNLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
Db 1 MKVLSLLYLLTAIFGILSDVOLQBSGPNLVKPSQSLSLTCTVTGYSITSGTYNNWIRQFP 60

QY 61 GNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
Db 61 GNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116

RESULT 4
HV62 MOUSE
ID HV62 MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 733 precursor.
OS Mus musculus (Mouse)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J070510; HVMS73.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 64.3%; Score 461.5; DB 1; Length 117;
Best Local Similarity 74.4%; Pred. No. 5.4e-38;
Matches 87; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 MRVLLILLWLTAFPGILSDVOLQBSGPNLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 59
Db 1 MKMFTLLYLLTWPGILSDVOLQBSGPNLVKPSQSLSLTCTVTGYSITSGTYNNWIRQFP 60

QY 60 PGNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
Db 61 PGNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 117

RESULT 5
HV47 MOUSE
ID HV47 MOUSE STANDARD; PRT; 113 AA.
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 36-60.
OS Mus musculus (Mouse)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
```

```
RC STRAIN=A/J;
RX MEDLINE=84024551; PubMed=6414509;
RA Juszcak E.C., Margolies M.N.;
RT "Amino acid sequence of the heavy chain variable region from the A/J
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
RT idio type.";
RL Biochemistry 22:4291-4296(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC STRAIN A/J MICE.
DR PIR; A02098; G2MS60.
DR PUB; L310; 18-FEB-03.
DR PUB; L31P; 18-FEB-03.
DR PUB; L31X; 18-FEB-03.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT NON TER 113
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

Query Match 62.7%; Score 450; DB 1; Length 113;
Best Local Similarity 74.8%; Pred. No. 6.8e-37;
Matches 89; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

QY 19 DVQLQESGPNLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMCYISGITYY 78
Db 1 EVQLQESGPNLVKPSQSLSLTCTVTGYSITSDY-WNNIRKFPGNKLEWMCYISGITYY 59

QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQTSVTVSS 137
Db 60 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQTSVTVSS 113

RESULT 6
HV43 MOUSE
ID HV43 MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; V00768; CAA24149.1; --
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
```

```
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 53.6%; Score 384.5; DB 1; Length 144;
Best Local Similarity 56.2%; Pred. No. 2e-30;
Matches 82; Conservative 22; Mismatches 31; Indels 11; Gaps 4;

QY 1 MRVLILLMLFTAPPG-ILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
Db 1 MAVLALLFLCLATFPSCILSQVLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
QY 60 PGNKLEWGWYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCA---- 115
Db 60 PCKGLEWLTGNGSTDYNTLKSLRTITKDNKSKQVFLKMNLSLQTDRTARYYCAVSII 119
QY 116 ----RSLARTTAMDYWGQGSTVTVSS 137
Db 120 YYGRS-DKYFLDYWGQGSTVTVSS 144

RESULT 7
HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RL repeat sequence in 5' flanking region.";
RL Gene 33:181-189 (1985).
DR PIR: A02101; GIH02.
DR HSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 127 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 52.6%; Score 377.5; DB 1; Length 146;
Best Local Similarity 56.7%; Pred. No. 9.5e-30;
Matches 80; Conservative 16; Mismatches 36; Indels 9; Gaps 2;

QY 5 ILLWLFTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNKL 64
Db 7 LLLWCQLPDVGLSQVLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNKL 65
QY 65 EWMGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCARSLAR---- 120
Db 66 EWICEINHSSTNYKTSLSKSRVTISLDTSKNLFSLSSVTAADTAVVYVYCARGLRGWN 125
QY 121 ----TTAMDYWGQGSTVTVSS 137
Db 126 DVYYYGMDVWGQGSTVTVSS 146

RESULT 8
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
ON NCBI_TaxID=8355;
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL: J03632; AAA49791.1; -
CC FIP: B31933; B31933.
CC HSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 47.1%; Score 338; DB 1; Length 135;
Best Local Similarity 50.7%; Pred. No. 5.7e-26;
Matches 68; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

QY 5 ILLWLFTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNKL 63
Db 3 IIFIFMFFSPCILSQTLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNKL 61
QY 64 LEWNGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCARSLARITA 123
Db 62 LEWIGVIATGGSTAIDSLKRNVTITKDNKKQVQLQNGMEVKDTAMYYCAREYASGYN 121
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SEQUENCE.
MEDLINE=70114712; PubMed=5264153;
Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
"Subgroups of amino acid sequences in the variable regions of
immunoglobulin heavy chains";
Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
-!- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02093; GIHUE.
HSSP; P01825; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00447; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin V region; PyroIridone carboxylic acid.
DOMAIN 1 120
FT MOD_RES 1 1
FT NON_TER 121 121
FT SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 45.0%; Score 323; DB 1; Length 121;
Best Local Similarity 52.5%; Pred. No. 1.4e-24;
Matches 63; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 20 VOLQESGPLVKRPSQSLSTCTVTGVSITSDH-AMSWIRQFPGNKLEWNGYISY-SGITT 77
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 2 VTLKENGPTLVKPTETLTCTLSGLSLTDTGVAVGIRQGPGRLEWLAWLLYDDDKR 61

QY 78 YNPSLKSRISITRDTSKNQFFQLQNSVTGDTSTIYCARSLLRTTAMDYWGQTSVTVSS 137
:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 62 FSPSLKSLRTLVTRDTSKNQVLTMTNMDDPVDATYCYVHRHPTLAFDVGWGQTKVAVSS 121

RESULT 13
HV45_MOUSE STANDARD; PRT; 116 AA.
ID HV45_MOUSE AC P01821;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MC101 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=82075900; PubMed=6273429;
Kataoka T., Nikaïdo T., Miyata T., Moriaki K., Honjo T.;
"The nucleotide sequences of rearranged and germline immunoglobulin
VH genes of a mouse myeloma MC101 and evolution of VH genes in
mouse.";
J. Biol. Chem. 257:277-285(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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EMBL; J00502; AAA38515.1; -.
DR PIR; A02096; GIMS10.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.
FT DOMAIN 20 >116 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

Query Match 44.0%; Score 316; DB 1; Length 116;
Best Local Similarity 53.8%; Pred. No. 6.5e-24;
Matches 63; Conservative 22; Mismatches 36; Indels 2; Gaps 2;

QY 1 MRVLTLMLFTAFPG-IISDVQLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROF 59
Db 1 MAVLGLLFLVTFPCVLVSQVQLKOSGGLVQPSQSLTCTVTGYSITSDHAWSWIROF 59
QY 60 PGNKLEWGYISGITYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
Db 60 PKGLEWLVGWSGSTDYNAFISRLSISKNSKQVFFKXNSLQSNDAIYYCAR 116

RESULT 14
HV01 XENLA
ID HV01 XENLA STANDARD; PRT; 136 AA.
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG8 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; M20484; AAA49774.1; ALT_TERM.
DR PIR; A31933; A31933.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT DOMAIN 19 128 IG-LIKE.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match 43.5%; Score 312.5; DB 1; Length 136;
Best Local Similarity 47.4%; Pred. No. 1.7e-23;
Matches 64; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 4 LILMLFTAFPGILSDVQLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFPGNK 63
Db 4 IFVIFMFSPSCILSQT-LQESGPGTVKPSSESLTCTVSGFELTSYYV-WIQPPRKT 61
QY 64 LEWNGYISGITYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLRTTA 123
Db 62 LEWIGVVRTDGTSTAIADSLKNRVTITKDNKGKQVYLQWNGMEVKDTAMYYCTSLAGTAG 121

QY 124 -MDYWGQGTSTVTVSS 137
Db 122 YFEHWGQGTMTVTTS 136

RESULT 15
HV2C HUMAN
ID HV2C HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; G1HUDW.
DR HSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 42.9%; Score 308; DB 1; Length 119;
Best Local Similarity 50.4%; Pred. No. 4e-23;
Matches 60; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

QY 20 VQLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFPGNKLEWGYISGITY 78
Db 2 VTLRESGPAIVRPQTTLTCTFSGSLSGTMCVMIROPPGGALEWLINDDKVY 61
QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLRTTAMDYWGQGTSTVTVSS 137
Db 62 GASLETRAVSKDTSKNQVLLMNTVPGDGTATYYCARSCG-SQYFDYWGQGLVTVSS 119

Search completed: October 22, 2003, 22:17:09
Job time : 14.0114 secs
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Db 61 GNKLEWMMGYINYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDATYYCA----- 115

QY 121 TTAMDY----WGQGTSTVSS 137  
Db 116 --SRGYSWFPNWGGTLTVSA 135

## RESULT 2

Q91X92  
ID Q91X92 PRELIMINARY; PRT; 482 AA.  
AC Q91X92; 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Unknown (Protein for MGC:18822).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011181; AAH11181.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 57.7%; Score 414; DB 11; Length 482;

Best Local Similarity 60.9%; Pred. No. 4e-34; Indels 2; Gaps 2;  
Matches 84; Conservative 19; Mismatches 33;

QY 1 MRVLLLLWLTAPPG-ILSDVQLQESGPLVKPQSLSLTCTVTGYSTSDHAWSWIQF 59  
Db 1 MAVLALLCLVTFPSCALSQVQLKESGPLVAPQSLSITCVSGFALTS-YAISWVRQP 59  
QY 60 PGNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQNLNVTTGDTSTYYCARSLA 119  
Db 60 PCKGLEWLGIWGTGVNYSALKSRLSISKNSKQVFLKNSLTQNTDARYCARDN 119  
QY 120 RTAMDYWGQGTSTVSS 137  
Db 120 YEGAMDYWGQGTSTVSS 137

## RESULT 3

Q96KX8  
ID Q96KX8 PRELIMINARY; PRT; 496 AA.  
AC Q96KX8; 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein\_  
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 54.8%; Score 393.5; DB 4; Length 496;

Best Local Similarity 60.0%; Pred. No. 5.3e-32;  
Matches 84; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

QY 7 LWLF---TAPP-GILSDVQLQESGPLVKPQSLSLTCTVTGYSI-TSDHAWSWIQPPG 61  
Db 4 LWFFLLVAAPRWLSQLQESGPLVKSETLSLTCTVSGSISSSSYWGIQPPG 63  
QY 62 NKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQNLNVTTGDTSTYYCAR---S 117  
Db 64 KGLEWANTYISGITYNPSLKSRISTRDTSKNQFLQNLNVTTGDTSTYYCARHGYSR 123  
QY 118 LARTAMDYWGQGTSTVSS 137  
Db 124 SGRTGADYWGQGTSTVSS 143

## RESULT 4

Q96EYO  
ID Q96EYO PRELIMINARY; PRT; 613 AA.  
AC Q96EYO; 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 53.8%; Score 386.5; DB 4; Length 613;

Best Local Similarity 61.3%; Pred. No. 3.6e-31;  
Matches 84; Conservative 15; Mismatches 31; Indels 7; Gaps 4;

QY 7 LWLF---TAPP-GILSDVQLQESGPLVKPQSLSLTCTVTGYSTSDHAWSWIQPPG 62  
Db 4 LWFFLLVAAPRWLSQLQESGPLVKSETLSLTCTVSGSISSSSYWGIQPPG 62  
QY 63 KLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQNLNVTTGDTSTYYCAR--LAR 120  
Db 63 GLEWIGRIYTSSTNYNPSLKSRISTRDTSKNQFLKLSVTAADTAVYICASQPWELP 122  
QY 121 TTAMDYWGQGTSTVSS 137  
Db 123 TVGLFYWGQGTSTVSS 139

## RESULT 5

Q9UL73  
ID Q9UL73 PRELIMINARY; PRT; 119 AA.  
AC Q9UL73; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 53.2%; Score 382; DB 4; Length 119;
Best Local Similarity 66.4%; Pred. No. 1.4e-31;
Matches 79; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 20 VQLQESGPGVLVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWNGYISYGITTYN 79
DB 2 VQLQESGPGVLVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWIGYIYSGSYNYT 60
QY 80 PSLSKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR-SLARTTAMDYWGQGSTVTVSS 137
DB 61 PSLSKRVTSIDRSKNQFSLKTLTAADTAVYFCARLSNWPYFYDYWGQGLTVTVSS 119

RESULT 6
ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IgM secreting B cell in the synovium of
RT Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >150 V4 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 52.1%; Score 374; DB 4; Length 597;
Best Local Similarity 56.3%; Pred. No. 6.7e-30;
Matches 80; Conservative 18; Mismatches 32; Indels 12; Gaps 4;

QY 7 LWLF---TAPP-GILSDVQLQESGPGVLVKPSQSLTCTVTGYSITSDHAWSWIRQPPGN 62
DB 4 LWFFLLLVAAPRWLSQLQESGPGVLVKPSQSLTCTVTGYSITSDHAWSWIRQPPGK 62
QY 63 KLEWNGYISYGITTYNPSLSKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTT 122
DB 63 GLEWIGEINHSGITTYNPSLSKRVTISVDTSKKQLSLKSSVNAADTAVYCARVITRAS 122
QY 123 -----AMDYWGQGSTVTVSS 137
DB 123 PGTDGRYGMVDVWGQGTITVTVSS 144

RESULT 8
ID Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RL Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019235; AAH19235.1;  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;  
 Query Match 51.3%; Score 368; DB 4; Length 588;  
 Best Local Similarity 55.6%; Pred. No. 2.7e-29;  
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;  
 QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYTSDHAWSWIRQFPGN 62  
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGSF-SCGYWWSWIRQFPGK 62  
 QY 63 KLEWGWISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTT 122  
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDVTSSKQLSLSSVNAADTAVYYCARVITRAS 122  
 QY 123 -----AMDYWGQGTSTVTVSS 137  
 DB 123 PGTDGRYGMVWVGQGTITVTVSS 144  
 RESULT 9  
 ID Q9BU10 PRELIMINARY; PRT; 597 AA.  
 AC Q9BU10;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RL Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002963; AAH02963.1;  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;  
 Query Match 51.3%; Score 368; DB 4; Length 597;  
 Best Local Similarity 55.6%; Pred. No. 2.8e-29;  
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;  
 QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYTSDHAWSWIRQFPGN 62  
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGSF-SCGYWWSWIRQFPGK 62

QY 63 KLEWGWISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTT 122  
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDVTSSKQLSLSSVNAADTAVYYCARVITRAS 122  
 QY 123 -----AMDYWGQGTSTVTVSS 137  
 DB 123 PGTDGRYGMVWVGQGTITVTVSS 144  
 RESULT 10  
 ID Q96AA6 PRELIMINARY; PRT; 618 AA.  
 AC Q96AA6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RL Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC017356; AAH17356.1;  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;  
 Query Match 51.3%; Score 368; DB 4; Length 618;  
 Best Local Similarity 55.6%; Pred. No. 2.9e-29;  
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;  
 QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYTSDHAWSWIRQFPGN 62  
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGSF-SCGYWWSWIRQFPGK 62  
 QY 63 KLEWGWISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTT 122  
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDVTSSKQLSLSSVNAADTAVYYCARVITRAS 122  
 QY 123 -----AMDYWGQGTSTVTVSS 137  
 DB 123 PGTDGRYGMVWVGQGTITVTVSS 144  
 RESULT 11  
 ID Q99NG4 PRELIMINARY; PRT; 121 AA.  
 AC Q99NG4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Single chain Fv (Fragment).  
 OS Mus musculus (Mouse).  
 OG Plasmid PHEN1.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=98169018; PubMed=9510199;  
 RA Hawlich H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,  
 Bautsch W., Kola A., Kios A., Koehl J.;







GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 22, 2003; 22:14:35 ; Search time 14.5303 Seconds  
(without alignments)  
398.931 Million cell updates/sec

Title: US-09-114-285A-31

Perfect score: 718

Sequence: 1 MRVLLILWLFTAFPGILSDV.....LARTAMDYWGQGTSTVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 718   | 100.0       | 137    | 1  | US-08-137-117D-31 |
| 2          | 718   | 100.0       | 137    | 2  | US-08-436-717-31  |
| 3          | 538   | 74.9        | 138    | 1  | US-08-137-117D-69 |
| 4          | 538   | 74.9        | 138    | 2  | US-08-436-717-69  |
| 5          | 534   | 74.4        | 119    | 3  | US-08-767-128-18  |
| 6          | 534   | 74.4        | 130    | 3  | US-08-466-151-5   |
| 7          | 534   | 74.4        | 130    | 4  | US-08-466-163B-5  |
| 8          | 527   | 73.4        | 123    | 1  | US-08-137-117D-64 |
| 9          | 527   | 73.4        | 123    | 2  | US-08-436-717-64  |
| 10         | 518.5 | 72.2        | 240    | 2  | US-07-956-399-2   |
| 11         | 500.5 | 69.7        | 114    | 1  | US-08-111-080-23  |
| 12         | 500.5 | 69.7        | 114    | 1  | US-08-211-980-23  |
| 13         | 500.5 | 69.7        | 114    | 5  | PCT-US93-07967-23 |
| 14         | 499   | 69.5        | 213    | 4  | US-09-170-769A-2  |
| 15         | 496   | 69.1        | 118    | 3  | US-09-065-059-11  |
| 16         | 493   | 68.7        | 117    | 2  | US-08-672-345C-13 |
| 17         | 493   | 68.7        | 117    | 3  | US-09-214-095D-13 |
| 18         | 491.5 | 68.5        | 117    | 2  | US-08-308-494A-13 |
| 19         | 478.5 | 66.6        | 241    | 3  | US-08-902-486-13  |
| 20         | 478.5 | 66.6        | 496    | 3  | US-08-902-486-15  |
| 21         | 475.5 | 66.2        | 638    | 3  | US-09-070-637-20  |
| 22         | 468.5 | 65.3        | 137    | 3  | US-08-466-151-7   |
| 23         | 468.5 | 65.3        | 137    | 4  | US-08-466-163B-7  |
| 24         | 468   | 65.2        | 113    | 1  | US-08-107-669D-5  |
| 25         | 468   | 65.2        | 113    | 1  | US-08-472-788A-5  |
| 26         | 468   | 65.2        | 113    | 2  | US-08-477-531B-5  |
| 27         | 468   | 65.2        | 113    | 2  | US-08-082-842A-5  |

Sequence 14, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 100, App  
Sequence 101, App  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 102, App  
Sequence 106, App  
Sequence 119, App  
Sequence 12, Appl  
Sequence 102, App  
Sequence 12, Appl  
Sequence 103, App  
Sequence 110, App  
Sequence 2, Appli  
Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-137-117D-31  
; Sequence 31, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 137 amino acids  
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-31

Query Match      100.0%; Score 718; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVILLLLWLTAFPGILSDVQLQESGPNLVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
DB 1 MRVILLLLWLTAFPGILSDVQLQESGPNLVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
QY 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQGTSTVTVSS 137
DB 121 TTAMDYWGQGTSTVTVSS 137

RESULT 2
US-08-436-717-31
; Sequence 31, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-69

Query Match      100.0%; Score 718; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVILLLLWLTAFPGILSDVQLQESGPNLVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
DB 1 MRVILLLLWLTAFPGILSDVQLQESGPNLVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
QY 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQGTSTVTVSS 137
DB 121 TTAMDYWGQGTSTVTVSS 137

RESULT 3
US-08-137-117D-69
; Sequence 69, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-18

Query Match          74.4%; Score 534; DB 3; Length 119;
Best Local Similarity 85.7%; Pred. No. 4.7e-47;
Matches 102; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGVLVKPSQSLTCTVTGYSTSDYANNWIRQPGNKLEWNGYISYSGITSY 60

QY 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGSTVTYSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCARCGNYPWFYDWGQGTTLTVSS 119

RESULT 6
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P07182C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

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Query Match          74.4%; Score 534; DB 3; Length 130;
Best Local Similarity 86.6%; Pred. No. 5.3e-47;
Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGVLVKPSQSLTCTVTGYSTSDANNWIRQPGNKLEWNGYINHSGTTSY 60

QY 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGSTVTYSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCAMVVA--YAMDYWGQGSTVTYSS 117

RESULT 7
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P07182C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Query Match          74.4%; Score 534; DB 4; Length 130;
Best Local Similarity 86.6%; Pred. No. 5.3e-47;
Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGVLVKPSQSLTCTVTGYSTSDANNWIRQPGNKLEWNGYINHSGTTSY 60

QY 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGSTVTYSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCAMVVA--YAMDYWGQGSTVTYSS 117

RESULT 8
US-08-137-117D-64
; Sequence 64, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

```



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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ohlon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248955 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-2

Query Match 72.2%; Score 518.5; DB 2; Length 240;
Best Local Similarity 82.5%; Pred. No. 4.4e-45;
Matches 99; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 18 SDVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITT 77
Db 122 TQVKLEESGPGVLVKPSQSLTCTVTGYPIITSDYAMDWIRQPPGNKLEWGMGVIYSYGSTD 181
QY 78 YNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTTAMDYWGOGTSTVTVSS 137
Db 182 YNPSLKSRISIRDSIKNOFFLQLNSVTTEDTATYYCARG-GFPYAMDYWGOGTSTVTVSS 240

RESULT 11
US-08-111-080-23
; Sequence 23, Application 08/111080
; Patent No. 555865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-080-23

Query Match 69.7%; Score 500.5; DB 1; Length 114;
Best Local Similarity 81.5%; Pred. No. 1.1e-43;
Matches 97; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 19 DVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITT 78
Db 1 EVQLQESGPGVLVKPSQSLTCTVTGYISITSDYAMNIRQPPGNKLEWGMGVIYSYGSTTY 60
QY 79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTTAMDYWGOGTSTVTVSS 137
Db 61 NPSLKSRISITRDTSKNLFLLQLSSVTSEDATYYCARG-----SFGDWGOGTLLTVTSA 114

RESULT 12
US-08-211-980-23
; Sequence 23, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-980-23

Query Match 69.7%; Score 500.5; DB 1; Length 114;
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; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-065-059-11

Query Match 69.1%; Score 496; DB 3; Length 118;  
Best Local Similarity 79.7%; Pred. No. 3 4e-43;  
Matches 94; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
QY 20 VOLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIRQFPGNKLWNGYISYSGITTYN 79  
Db 1 VOLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIRQFPGNKLWNGYISYSGITTYN 60  
QY 80 PSLKSRISITRDTSKNQFLQNSVTGDTSTYYCARSLARTTANDYWGQTSVTSS 137  
Db 61 PSLKSRISITRDTSKNQFLQNSVTGDTSTYYCARSLARTTANDYWGQTSVTSS 118

Search completed: October 22, 2003, 22:20:50  
Job time : 15.5303 secs

| Result No. | Score | Query Match | Length | DB | ID                | Description |
|------------|-------|-------------|--------|----|-------------------|-------------|
| 1          | 534   | 74.4        | 130    | 9  | US-09-802-077-5   | Sequence 5  |
| 2          | 534   | 74.4        | 130    | 9  | US-09-802-096-5   | Sequence 5  |
| 3          | 534   | 74.4        | 130    | 11 | US-09-925-179-5   | Sequence 5  |
| 4          | 521   | 72.6        | 115    | 10 | US-09-144-886-58  | Sequence 5  |
| 5          | 521   | 72.6        | 121    | 12 | US-10-310-674A-36 | Sequence 1  |
| 6          | 518   | 72.1        | 115    | 10 | US-09-144-886-59  | Sequence 5  |
| 7          | 512.5 | 71.4        | 140    | 11 | US-09-874-141-53  | Sequence 5  |
| 8          | 499.5 | 69.6        | 118    | 15 | US-10-184-300A-3  | Sequence 5  |
| 9          | 498   | 69.4        | 266    | 15 | US-10-207-685-380 | Sequence 2  |
| 10         | 498   | 69.4        | 550    | 15 | US-10-207-685-270 | Sequence 2  |
| 11         | 497.5 | 69.3        | 136    | 9  | US-09-858-349-2   | Sequence 2  |
| 12         | 494   | 68.8        | 119    | 15 | US-10-207-655-358 | Sequence 2  |
| 13         | 493   | 68.7        | 117    | 11 | US-09-940-727B-13 | Sequence 1  |
| 14         | 476.5 | 66.4        | 118    | 10 | US-10-184-300A-2  | Sequence 2  |
| 15         | 476.5 | 66.4        | 140    | 11 | US-09-874-141-49  | Sequence 4  |

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 2

US-09-802-096-5

; Sequence 5, Application US/09802096

; Patent No. US2001003839A1

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

; FILE REFERENCE: P07182C3US

; CURRENT APPLICATION NUMBER: US/09/802,096

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-802-096-5

Query Match 74.4%; Score 534; DB 9; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 19 DVQLQESGVLVKPQSLSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGYSIGITTY 78

Db 1 DVQLQESGVLVKPQSLSLTCTVTGYITSDNANNWIRQPPGNKLEWGMGYNHSGTTSY 60

Qy 79 NPSLKSRSITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 3

US-09-925-179-5

; Sequence 5, Application US/09925179

; Publication No. US20030044858A1

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)

; FILE REFERENCE: P07182C1D1C1US

; CURRENT APPLICATION NUMBER: US/09/925,179

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-925-179-5

Query Match 74.4%; Score 534; DB 9; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 19 DVQLQESGVLVKPQSLSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGYSIGITTY 78

Db 1 DVQLQESGVLVKPQSLSLTCTVTGYITSDNANNWIRQPPGNKLEWGMGYNHSGTTSY 60

Qy 79 NPSLKSRSITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

Query Match 74.4%; Score 534; DB 11; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 19 DVQLQESGVLVKPQSLSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGYSIGITTY 78

Db 1 DVQLQESGVLVKPQSLSLTCTVTGYITSDNANNWIRQPPGNKLEWGMGYNHSGTTSY 60

Qy 79 NPSLKSRSITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 4

US-09-144-886-58

; Sequence 58, Application US/09144886

; Patent No. US20020155114A1

; GENERAL INFORMATION:

; APPLICANT: Marks, James D

; APPLICANT: Amersdorfer, Peter

; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize

; TITLE OF INVENTION: Botulinum Neurotoxins

; FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144,886

; CURRENT FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 115

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone

; OTHER INFORMATION: I18 region VH epitope 1

US-09-144-886-58

Query Match 72.6%; Score 521; DB 10; Length 115;

Best Local Similarity 86.6%; Pred. No. 5.7e-42;

Matches 103; Conservative 3; Mismatches 9; Indels 4; Gaps 2;

Qy 19 DVQLQESGVLVKPQSLSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGYSIGITTY 78

Db 1 EVQLQESGVLVKPQSLSLTCTVTGYISIT-DYAMNWIROPFGKLEWGMGYSISGSTGY 59

Qy 79 NPSLKSRSITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTSS 137

Db 60 NPSLKSRSITRDTSKNQFFLQNSVTTEDTGYTCARGY---DAMDYWGQGTSTVTSS 115

RESULT 5

US-10-310-674A-36

; Sequence 36, Application US/10310674A

; Publication No. US20030166860A1

; GENERAL INFORMATION:

; APPLICANT: TeGenero GmbH

; TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor

; TITLE OF INVENTION: Family

; FILE REFERENCE: 00140/004001

; CURRENT APPLICATION NUMBER: US/10/310,674A

; CURRENT FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 36

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: No. US20030166860A1e1 Sequence

US-10-310-674A-36

Query Match 72.6%; Score 521; DB 12; Length 121;

Best Local Similarity 83.5%; Pred. No. 6e-42;

```
Matches 101; Conservative 6; Mismatches 12; Indels 2; Gaps 1;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLQESGVLVVKPSQSLTCTVTGYSITSDYAWNWIRQPPGNKLEWMGYIRYSGSTYS 60
Qy 79 NPSLKSRISTRDTSKNQFFLQNLNSVTTGDTSTYYCARSARTT--AMDYWGQGTSTVTS 136
Db 61 NPSLKSRISTRDTSKNQFFLQNLNSVTTEDTATYYCARDWPRPSYWFVDMVAGGTTVTS 120
Qy 137 S 137
Db 121 S 121

RESULT 6
US-09-144-886-59
; Sequence 59, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 59
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 167 region VH epitope 1
US-09-144-886-59

Query Match 72.1%; Score 518; DB 10; Length 115;
Best Local Similarity 86.6%; Pred. No. 1.1e-41;
Matches 103; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 EVQLQESGVLVVKPSQSLTCTVTGYSIT-DYAWYIRQPPGNKLEWMGYISYSGSTGY 59
Qy 79 NPSLKSRISTRDTSKNQFFLQNLNSVTTGDTSTYYCARSARTTAMDYWGQGTSTVTS 137
Db 60 NPSLKSRISTRDTSKNQFFLQNLNSVTTEDTGTTCARGY---DAMDYWGQGTSTVTS 115

RESULT 7
US-09-874-141-53
; Sequence 53, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 53
; LENGTH: 140
; TYPE: PRT
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```
; ORGANISM: Homo sapiens
US-09-874-141-53

Query Match 71.4%; Score 512.5; DB 11; Length 140;
Best Local Similarity 75.5%; Pred. No. 4.5e-41;
Matches 105; Conservative 12; Mismatches 19; Indels 3; Gaps 3;
Qy 1 MRVLILWLFTAPPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPP 60
Db 1 MVLVLLYLLTALPGFLSEVQLQESGVLVVKPSQSLTCTVTGDSITNGF-MIWIIRKFP 59
Qy 61 GNKLEWMGYISYSGITTYNPSLSKRSISITRDTSKNQFFLQNLNSVTTGDTSTYYCA-RSLA 119
Db 60 GNKLEYMGYISYSGSTYVNPSPSKRSISITRDTSQNQFLQNLNSVTTEDTCTYYCACRSYG 119
Qy 120 RTT-AMDYWGQGTSTVTS 137
Db 120 RTPYDFWQGGTTLTVSS 138

RESULT 8
US-10-184-300A-3
; Sequence 3, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184,300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().7)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv7
US-10-184-300A-3

Query Match 69.6%; Score 499.5; DB 15; Length 118;
Best Local Similarity 79.0%; Pred. No. 6.4e-40;
Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLKESGVLVVKPTQTTLTCTVTGYSITSDYAWNWIRQPPGNKLEWMGYITYSGTTSY 60
Qy 79 NPSLKSRISTRDTSKNQFFLQNLNSVTTGDTSTYYCARSARTTAMDYWGQGTSTVTS 137
Db 61 NPSLTSRISISRDTSKNQFFLQNLNSVTSBTDATYYCAREWF-PYYFDYWGQGTTLTVSS 118

RESULT 9
US-10-207-655-260
; Sequence 260, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
```

```
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 260
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-260

Query Match          69.4%; Score 498; DB 15; Length 266;
Best Local Similarity 79.2%; Pred. No. 2.2e-39;
Matches 95; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 18 SDVQLQESGPVLVKPSQSLTCTVTGYSTSDHAWSIROPFGNKLWGMGVIYSGIT 77
Db 146 SDVQLQESGPGLVKPSQSLTCSVTGYSTSGFYNNWIRQPPGNKLWGMGHISHDGRNN 205

QY 78 YNPISLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
Db 206 YNPISLNRISITRDTSKNQFFLKLSSVTEDTATYFCARHYGSSGAMDYWGQGTSTVTVSS 265

RESULT 10
US-10-207-655-270
; Sequence 270, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 270
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-270

Query Match          69.4%; Score 498; DB 15; Length 550;
Best Local Similarity 79.2%; Pred. No. 5.1e-39;
Matches 95; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 18 SDVQLQESGPVLVKPSQSLTCTVTGYSTSDHAWSIROPFGNKLWGMGVIYSGIT 77
Db 146 SDVQLQESGPGLVKPSQSLTCSVTGYSTSGFYNNWIRQPPGNKLWGMGHISHDGRNN 205

QY 78 YNPISLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
Db 206 YNPISLNRISITRDTSKNQFFLKLSSVTEDTATYFCARHYGSSGAMDYWGQGTSTVTVSS 265

RESULT 11
US-09-858-349-2
; Sequence 2, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFVTI peptide
```

```
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (99)..(107)
; OTHER INFORMATION: variable
US-09-858-349-2

Query Match          69.3%; Score 497.5; DB 9; Length 136;
Best Local Similarity 78.3%; Pred. No. 1.2e-39;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 19 DVQLQESGPVLVKPSQSLTCTVTGYSTSDHAWSIROPFGNKLWGMGVIYSGITTY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGFYNNWIRQPPGNKLWGMGVIYSDGSNNY 60

QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCAR-SLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLNRISITRDTSKNQFFLKLSSVTEDTATYFCARHYGSSGAMDYWGQGTSTVTVAA 120

RESULT 12
US-10-207-655-258
; Sequence 258, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-258

Query Match          68.8%; Score 494; DB 15; Length 119;
Best Local Similarity 79.0%; Pred. No. 2.1e-39;
Matches 94; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 19 DVQLQESGPVLVKPSQSLTCTVTGYSTSDHAWSIROPFGNKLWGMGVIYSGITTY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGFYNNWIRQPPGNKLWGMGHISHDGRNNY 60

QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLNRISITRDTSKNQFFLKLSSVTEDTATYFCARHYGSSGAMDYWGQGTSTVTVSS 119

RESULT 13
US-09-940-727B-13
; Sequence 13, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 117
```

```

; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-13

Query Match      68.7%; Score 493; DB 11; Length 117;
Best Local Similarity 78.5%; Pred. No. 2.6e-39;
Matches 95; Conservative 8; Mismatches 6; Indels 12; Gaps 2;

Qy 19 DVQLQESGPELVKPSQSLSLTCTVTGYISITSDHAWMIROPPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGPELVKPSQSLSLTCTVTGYISITSDYANNWIRQPPGNRLEWNGYIRYSGITRY 60

Qy 79 NPSLKSRIISIRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDY-----WGQTSV 133
Db 61 NPSLKSRIISIRDTSKNQFFLQNSVTTEDTATYTCVR-----IHVYGYGNWGQQTTL 113

Qy 134 T 134
Db 114 T 114

RESULT 14
US-10-184-300A-2
; Sequence 2, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Cart, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184.300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv6
US-10-184-300A-2

Query Match      66.4%; Score 476.5; DB 15; Length 118;
Best Local Similarity 76.5%; Pred. No. 9.6e-38;
Matches 91; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

Qy 19 DVQLQESGPELVKPSQSLSLTCTVTGYISITSDHAWMIROPPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGPELVKPSQSLSLTCTVTGYISITSDYANNWIRQPPGNKLEWNGYITYSGITSY 60

Qy 79 NPSLKSRIISIRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQTSVTVSS 137
Db 61 NPSLTSRISIRDTSKNQFFLQNSVTSIEDTATYTCAREWF-PYVFDYWGQQTTLTVSS 118

RESULT 15
US-09-874-141-49
; Sequence 49, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.

```

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; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 49
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized VH#1 amino acid
US-09-874-141-49

Query Match      66.4%; Score 476.5; DB 11; Length 140;
Best Local Similarity 71.2%; Pred. No. 1.2e-37;
Matches 99; Conservative 14; Mismatches 23; Indels 3; Gaps 3;

Qy 1 MRVLIILLWLFAPFGILSDVQLQESGPELVKPSQSLSLTCTVTGYISITSDHAWMIROPP 60
Db 1 MMVLSLLYLLTALPGFLSEVQLQESGPELVKPSQSLSLTCTVTGYISITSDHAWMIROPP 59

Qy 61 GNKLEWNGYISYSGITTYNPSLKSRIISIRDTSKNQFFLQNSVTTGDTSTYTCARSLA 119
Db 60 GNKLEWNGYISYSGITTYNPSLKSRIISIRDTSKNQFFLQNSVTTGDTSTYTCARSLA 119

Qy 120 RTT-AMDYWGQTSVTVSS 137
Db 120 RTPVYFDYWGQQTTLTVSS 138

Search completed: October 22, 2003, 22:21:46
Job time : 26.428 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:57:16 ; Search time 976.125 Seconds  
(without alignments)  
1129.179 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATGAGAGTGTGATTCTTTT.....CCTCAGTCACCGTCTCTCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 281.2 | 68.4        | 1420   | 9  | US-09-237-061-2    |
| 2          | 278.6 | 67.8        | 363    | 12 | US-10-310-674A-35  |
| 3          | 271.4 | 66.0        | 806    | 14 | US-10-207-655-259  |
| 4          | 271.4 | 66.0        | 1665   | 14 | US-10-207-655-269  |
| 5          | 269   | 65.5        | 354    | 14 | US-10-184-300A-9   |
| 6          | 268   | 65.2        | 362    | 14 | US-10-207-655-257  |
| 7          | 260.8 | 63.5        | 411    | 9  | US-09-858-349-1    |
| 8          | 259.4 | 63.1        | 354    | 14 | US-10-184-300A-8   |
| 9          | 258.2 | 62.8        | 366    | 11 | US-09-940-727B-101 |
| 10         | 257.8 | 62.7        | 354    | 14 | US-10-184-300A-7   |
| 11         | 255.8 | 62.2        | 426    | 11 | US-09-874-141-52   |
| 12         | 255.8 | 62.2        | 426    | 12 | US-10-171-681-28   |
| 13         | 255.8 | 62.2        | 426    | 12 | US-10-171-680-28   |
| 14         | 253.4 | 61.7        | 366    | 11 | US-09-940-727B-105 |
| 15         | 245.6 | 59.8        | 420    | 11 | US-09-940-727B-109 |
| 16         | 245.4 | 59.7        | 419    | 11 | US-09-940-727B-113 |
|            |       |             |        |    | Sequence 2, Appl   |
|            |       |             |        |    | Sequence 35, Appl  |
|            |       |             |        |    | Sequence 259, App  |
|            |       |             |        |    | Sequence 269, App  |
|            |       |             |        |    | Sequence 9, Appli  |
|            |       |             |        |    | Sequence 257, App  |
|            |       |             |        |    | Sequence 1, Appli  |
|            |       |             |        |    | Sequence 8, Appli  |
|            |       |             |        |    | Sequence 101, App  |
|            |       |             |        |    | Sequence 7, Appli  |
|            |       |             |        |    | Sequence 52, Appl  |
|            |       |             |        |    | Sequence 28, Appl  |
|            |       |             |        |    | Sequence 28, Appl  |
|            |       |             |        |    | Sequence 105, App  |
|            |       |             |        |    | Sequence 109, App  |
|            |       |             |        |    | Sequence 113, App  |

#### ALIGNMENTS

#### RESULT 1

US-09-237-061-2  
; Sequence 2, Application US/09237061  
; Patent No. US20020081624A1  
; GENERAL INFORMATION:  
; APPLICANT: DuPont Pharmaceuticals Company  
; TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin  
; FILE OF INVENTION: Antagonist/Agonist Mediated Disease States  
; FILE REFERENCE: DM-6956  
; CURRENT APPLICATION NUMBER: US/09/237,061  
; CURRENT FILING DATE: 1999-01-26  
; PRIOR FILING DATE: 1999-01-26  
; PRIOR FILING DATE: 1998-01-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1420  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Heavy Chain of  
; OTHER INFORMATION: rUK094  
US-09-237-061-2

Query Match 68.4%; Score 281.2; DB 9; Length 1420;  
Best Local Similarity 81.6%; Pred. No. 8e-84;  
Matches 338; Conservative 0; Mismatches 73; Indels 3; Gaps 1;  
Qy 1 ATGAGAGTGTGATTCTTTTGGCTGCTTCACAGCCTTCTGTATCTCTGTCTGTGATGTG 60  
Db 14 ATGAAAGTGTGTGATCTGTGTACCTGTTGACAGCCATTCTGTGATCTCTGTGATGTA 73  
Qy 61 CAGCTTCAGGAGTCGGACCTGTCTCGTGAAGCTTCTCAGTCTCTGTCCCTCACCTGC 120  
Db 74 CAGCTTCAGGAGTCAGACCTGTGCTGTGAACCTTCTCAGTCTCTGTCTCACCTGC 133  
Qy 121 ACTGTCACTGGCTACTCAATCACAGTGATCATGCCGTGGAGTCGGAGTCGGAGATTCCA 180  
Db 134 TCTGTCACTGGCTACTCCATCACCAGTGGTATTACTTACTGGAACCTGGATCGGCAATTCCA 193

QY 181 GGAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACAACCA 240  
DB 194 GGAACAACTGGAGTGGGTACATAAGTTATGTCGGTAACTAGTACTACAACCA 253  
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTCTTCTCTACAG 300  
DB 254 TCTCTCAAAAGTCGAATCTCTATCACTCGTGAACATCTAAGAACCAAGTCTTCTCTGAAG 313  
QY 301 TTGAATTTCTGTACTACTGGGACACAGTCCACATATTACTGTGCAAGATCCCTAG---CT 357  
DB 314 TTGAATTTCTGTACTACTGGGACACAGTCCACATATTACTGTGCAAGATAGAGGGTAT 373  
QY 358 CGGACTACGGCTATGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCA 411  
DB 374 GACCACGGGGGTTTCTTACTGGGCAAGGACTCTGGTCACTGTCTCTGCA 427

## RESULT 2

US-10-310-674A-35  
; Sequence 35, Application US/10310674A  
; Publication No. US20030166860A1  
; GENERAL INFORMATION:  
; APPLICANT: Tegenero GmbH  
; TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor  
; FILE OF INVENTION: Family  
; FILE REFERENCE: 00140/004001  
; CURRENT APPLICATION NUMBER: US/10/310,674A  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 35  
; LENGTH: 363  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: No. US20030166860A1el Sequence  
US-10-310-674A-35

Query Match 67.8%; Score 278.6; DB 12; Length 363;

Best Local Similarity 87.6%; Pred. No. 3.3e-83;  
Matches 318; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 55 GATGTGCAGCTTCAGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 114  
DB 1 GATGTGCAGCTTCAGAGTCGGGACCTGCGCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 60  
QY 115 ACCTGCAGTCTCACTGGCTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCGGCGAG 174  
DB 61 ACCTGCAGTCTCACTGGCTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCGGCGAG 120  
QY 175 TTTCAGGAAACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTAC 234  
DB 121 TTTCAGGAAACAACTGGAGTGGATGGGCTACATAAGTACAGTGGTATCACTACCTAC 180  
QY 235 AACCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTCTTCTC 294  
DB 181 AATCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTCTTCTC 240  
QY 295 CTACAGTTGAATTTCTGTACTACTGGGACACGTCACATATTTACTGTGCAAGA----- 348  
DB 241 CTGAGTTGAATTTCTGTACTACTGGGACACACGTCACATATTTACTGTGCAAGATGG 300  
QY 349 TCCCTAGCTCGAGTACGCTATGAGTACTTGGGGTCAAGAACCTCAGTCACTCGCTTCC 408  
DB 301 CGCGACCGAGTACTGTGTACTTCAATGTCTGGGCGCAGGACCAACCGTCACTCGCTTCC 360  
QY 409 TCA 411  
DB 361 TCA 363

## RESULT 3

US-10-207-655-259  
; Sequence 259, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 259  
; LENGTH: 806  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polynucleotide  
US-10-207-655-259

Query Match 66.0%; Score 271.4; DB 14; Length 806;  
Best Local Similarity 83.5%; Pred. No. 1.2e-80;  
Matches 308; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 42 TGGTATCCTGCTCTCATGTGCAGCTTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCA 101  
DB 432 TGGCGCGGATCTCATGTACAGCTTTCAGGAGTCAGGACCTGGCCTCGTGAACCTTCTCA 491  
QY 102 GTCTCTGCTCCTACCTGCACTGTCTGCTGCTACTTCAATCAACAGTATCATGCTGTGAG 161  
DB 492 GTCTCTGCTCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551  
QY 162 CTGGATCGGAGTTCAGGAAACAACTGGAGTGGGCTACATAGTTACAGTGG 221  
DB 552 CTGGATCGGAGTTCAGGAAACAACTGGAGTGGGCTACATAGTTACAGTGG 611  
QY 222 TATCACTACCTACAAACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCAAA 281  
DB 612 TAGGAATACTACAAACCATCTCTCATATAAATCGAATCTCCATCACTCGTGACATCTAA 671  
QY 282 GAACAGTCTTCTCACTGAGTTGAATTTCTGAGTACTTGGGGACACGTCACATATTACTG 341  
DB 672 GAACAGTCTTCTCACTGAGTTGAGTTCTGTGACTACTGAGGACACAGTACATATTTCTG 731  
QY 342 TGAAGATCCCTAGCTCGGACTCGGATGAGTATGGGTCAGGCTGAGGTCAGGAACTCAGTCAC 401  
DB 732 TGAAGATCCCTAGCTCGGACTCGGATGAGTATGGGTCAGGCTGAGGTCAGGTCAGTCAC 791  
QY 402 CGTCTCTCTC 410  
DB 792 CGTCTCTCTC 800

## RESULT 4

US-10-207-655-269  
; Sequence 269, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 269  
; LENGTH: 1665  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polynucleotide  
US-10-207-655-269



; GENERAL INFORMATION:  
; APPLICANT: PLAKSIN, Daniel  
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS  
; FILE REFERENCE: 87534-2800  
; CURRENT APPLICATION NUMBER: US/09/858,349  
; CURRENT FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 411  
; TYPE: DNA  
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFV7I peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (295)..(320)  
; OTHER INFORMATION: a or g or c or t/u  
US-09-858-349-1

Query Match 63.5%; Score 260.8; DB 9; Length 411;  
Best Local Similarity 82.3%; Pred. No. 3.4e-77;  
Matches 293; Conservative 6; Mismatches 54; Indels 3; Gaps 1;  
  
Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCCTTCAGTCTCTGTCCTC 114  
Db 1 GATGCCAGCTCGAGAGTCAGGACCTGGCCCTCGTGAACCTTCTCAGTCTCTGTCCTC 60  
  
Qy 115 ACCTGCAGTGTCACTGGCTACTCAATCACCAGTGTATGCTGAGCTGGATCCGGCAG 174  
Db 61 ACCTGCAGTGTCACTGGCTACTCAATCACCAGTGTATGCTGGAAGTGGATCGGCAG 120  
  
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 234  
Db 61 ACCTGCAGTGTCACTGGCTACTCCATCACCAGTGGTTATTCTGGAAGTGGATCGGCAG 120  
  
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 234  
Db 121 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 180  
  
Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCCAGTTCTTC 294  
Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCTCTCGGACACATCCAAGAACCCAGTTCTTC 240  
  
Qy 295 CTACAGTTGAATTCCTGACCTACTCGGACACGTCCTCCACATATTACTGTGCAAGATCCCTA 354  
Db 241 CTGAGTTGAATTCCTGACCTCTTGAGGACACGCCACATATTACTGTGCAAGAGTGG 300  
  
Qy 355 GCTCGGACTACGGGTATGGACTACTTGGGGTCAAGAAACCTCAGTCACCGTCTCTCA 411  
Db 301 TTTC--CTTACTACTTGTACTACTTGGGGCCAGGCACCACTCTCACAGTCTCTTCA 354

RESULT 8  
US-10-184-300A-8  
; Sequence 8, Application US/10184300A  
; Publication No. US20030124056A1  
; GENERAL INFORMATION:  
; APPLICANT: Carr, Francis J.  
; APPLICANT: Hamilton, Anita A.  
; TITLE OF INVENTION: Carrier molecules  
; FILE REFERENCE: 229752001700  
; CURRENT APPLICATION NUMBER: US/10/184,300A  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: PCT/AU02/00827  
; PRIOR FILING DATE: 2002-10-26  
; PRIOR APPLICATION NUMBER: US 60/301,154  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/300,947  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 354  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)

; OTHER INFORMATION: Synthetic construct of 3B6DIVHv6  
US-10-184-300A-8  
  
Query Match 63.1%; Score 259.4; DB 14; Length 354;  
Best Local Similarity 84.9%; Pred. No. 9.3e-77;  
Matches 303; Conservative 0; Mismatches 51; Indels 3; Gaps 1;  
  
Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCCTTCTCAGTCTCTGTCCTC 114  
Db 1 GATGTGAGCTTAAGGAGTCGGGACCTGGCTGGTTAAACCTACTCAGACTCTGACCCCTC 60  
  
Qy 115 ACCTGCAGTGTCACTGGCTACTCAATCACCAGTGTATGCTGAGCTGGATCCGGCAG 174  
Db 61 ACCTGCAGTGTCACTGGCTACTCAATCACCAGTGTATGCTGGAAGTGGATCGGCAG 120  
  
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 234  
Db 121 CCACGAGAAAGGAGTGGAGTGGCTACATAAACCTACAGTGGTACCAGTAGCTAC 180  
  
Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCCAGTTCTTC 294  
Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCTCTCGGACACATCCAAGAACCCAGTTCTTC 240  
  
Qy 295 CTACAGTTGAATTCCTGACCTACTCGGACACGTCCTCCACATATTACTGTGCAAGATCCCTA 354  
Db 241 CTGAGTTGAATTCCTGACCTCTTGAGGACACGCCACATATTACTGTGCAAGAGTGG 300  
  
Qy 355 GCTCGGACTACGGGTATGGACTACTTGGGGTCAAGAAACCTCAGTCACCGTCTCTCA 411  
Db 301 TTTC--CTTACTACTTGTACTACTTGGGGCCAGGCACCACTCTCACAGTCTCTTCA 354

RESULT 9  
US-09-940-727B-101  
; Sequence 101, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 101  
; LENGTH: 366  
; TYPE: DNA  
; ORGANISM: mouse  
US-09-940-727B-101  
  
Query Match 62.8%; Score 258.2; DB 11; Length 366;  
Best Local Similarity 84.9%; Pred. No. 2.4e-76;  
Matches 303; Conservative 0; Mismatches 48; Indels 6; Gaps 1;  
  
Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCCTTCTCAGTCTCTGTCCTC 114  
Db 1 GATGTGAGCTTCAGGAGTCGGGACCTGGCTGGTTAAACCTTCTCAGTCTCTGTCCTC 60  
  
Qy 115 ACCTGCAGTGTCACTGGCTACTCAATCACCAGTGTATGCTGAGCTGGATCCGGCAG 174  
Db 61 ACCTGCAGTGTCACTGGCAATTCATCACCAGTGTATGCTGGAAGTGGATCGGCAG 120  
  
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 234  
Db 121 TTTCAGGAAACAACTGGAGTGGATGGCTACATAAGGACCACTTATTTGGCAGTAGTAC 180  
  
Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCCAGTTCTTC 294

Db 181 AACCTCTCTCATAAGTCGAATCTCTATCTCGAGACAGTCCAAAGAACCAAGTCTTTC 240  
Qy 295 CTACAGTTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTA 354  
Db 241 CTGAGTTGGATTTCTGACTGCTGAGACACAGCCACATATTATTGTGAAGATATCAT 300  
Qy 355 GCTCGACTACGGCTATGACTACTGCGGTCAAGAACCTCAGTCACCGTCTCTCTCA 411  
Db 301 TACTACGGTTCGGCT-----TACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCA 351

RESULT 10

US-10-184-300A-7  
; Sequence 7, Application US/10184300A  
; Publication No. US20030124056A1  
; GENERAL INFORMATION:  
; APPLICANT: Cart, Francis J.  
; APPLICANT: Hamilton, Anita A.  
; TITLE OF INVENTION: Carrier molecules  
; FILE REFERENCE: 229752001700  
; CURRENT APPLICATION NUMBER: US/10/184.300A  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: PCT/AU02/00827  
; PRIOR FILING DATE: 2002-10-26  
; PRIOR APPLICATION NUMBER: US 60/301,154  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/300,947  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 354  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv5  
US-10-184-300A-7

Query Match 62.7%; Score 257.8; DB 14; Length 354;  
Best Local Similarity 84.6%; Pred. No. 3.2e-76;  
Matches 302; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

Qy 55 GATGTGACGCTTCAGGACTCGGACCTGCTCTGTGAGCCCTTCTCAGTCTCTGTCCTC 114  
Db 1 GATGTGACGCTTAAGGAGTCGGGACCTGGCTTGGTTAAACCTACTTCAGACTCTGACCC 60  
Qy 115 ACCTGCACTGCTCAGTGGCTCAATCACAGTGATCATGCTGGAGCTGGATCCGGCAG 174  
Db 61 ACCTGCACTGCTCAGTGGCTCAATCACAGTGATCATGCTGGAGCTGGATCCGGCAG 120  
Qy 175 TTTCAGGAACAAACTGGAGTGGGCTGACATAAGTTACAGTGGTATCAGTACCTAC 234  
Db 121 CCACAGGAAGGAGTGGAGTGGGCTGACATAACCTACAGTGGTACCACTAGCTAC 180  
Qy 235 AACCCATCTCTCAAGTCGATCTCTATCTACCTCGAGACATCCAGAACCACTTCTTC 294  
Db 181 AACCCATCTCTCAAGTCGATCTCTATCTCTCGGACACATCCAGAACCACTTCTTC 240  
Qy 295 CTACAGTTGAATTTCTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTA 354  
Db 241 CTGAGTTGAATTTCTGACTCTGAGACACAGCCACATATTACTGTGCAAGAGATGG 300  
Qy 355 GCTCGACTACGGCTATGACTACTGCGGTCAAGAACCTCAGTCACCGTCTCTCTCA 411  
Db 301 TTTC---CTTACTACTTTGACTACTGGGGCCAAGGACCCTCTCAGAGTCTCTTCA 354

RESULT 11

US-09-874-141-52  
; Sequence 52, Application US/09874141

; Publication No. US20030012781A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL  
; APPLICANT: PAN, LI-ZHEN  
; APPLICANT: HANNA, NABIL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: KLOETZER, WILLIAM S.  
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0280632  
; CURRENT APPLICATION NUMBER: US/09/874,141  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/209,584  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(426)  
US-09-874-141-52

Query Match 62.2%; Score 255.8; DB 11; Length 426;  
Best Local Similarity 79.4%; Pred. No. 1.6e-75;  
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

Qy 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCCTTCTGTGATCTCTGTGATGTG 60  
Db 7 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCCGGGTTTCTGTGTACAGAGTG 66  
Qy 61 CAGCTTCAGGAGTCGGGACCTGCTGGTGAAGCCTTCTCAGTCTCTGCTCCCTCACCTGC 120  
Db 67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAACCTTCTCAGACTCTGTCCCTCACCTGT 126  
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGSCAGTTTCCA 180  
Db 127 TCTGTCACTGGGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAATTTCCA 183  
Qy 181 GGAACAACTGGAGTGGGCTACATAGTTACAGTGGTATCAGTACCTACCTACCAACCA 240  
Db 184 GGAATAAATCTGAGTACATGGGCTACATAAGTTTACAGTGGTAGCACTTACTACAATCCA 243  
Qy 241 TCTCTCAAAGTCAATCTCTATCACCTGAGACACATCCAGAACCAAGTCTTCTCTACAG 300  
Db 244 TCTCTCAAGAGTCAATCTCCATCACCTCGGACACATCCAGAACCAAGTCTTACTACAA 303  
Qy 301 TTGAATTTCTGACTACTGGGGACACGTCACATATTACTGTGCTGCTCCGCGAGTTACGGG 363  
Db 304 TTGAATTTCTGACTACTGAGGACACAGGCACATATTACTGTGCTGCTCCGCGAGTTACGGG 363  
Qy 361 ACTACGGC-----TATGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCA 411  
Db 364 AGGACCCCGTACTACTTTGACTTCTGGGGCCAAGGACCACCTCTCAGCGTCTCTCTCA 420

RESULT 12

US-10-171-681-28  
; Sequence 28, Application US/10171681  
; Publication No. US20030170233A1  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, Amelia  
; APPLICANT: HANNA, Nabil  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: NEWMAN, Roland A.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404



|     |   |     |
|-----|---|-----|
| 301 | TTGAATCTGTGACTACTCTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG | 360 |
| Qy  |   |     |
| 304 | TTGAATCTGTGACTACTGTGAGACACAGGCATATTACTGTGCTGCCGCAAGTTACGGG  | 363 |
| Db  |   |     |
| 361 | ACTACGGC-----TATGGACTCTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA    | 411 |
| Qy  |   |     |
| 364 | AGGACCCCGTACTACTTTTGACTTCTGGGGCAAGGCACCACTCTCACGTCCTCTCA    | 420 |
| Db  |   |     |

RESULT 14

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US-09-940-727B-105
; Sequence 105, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 366
; TYPE: DNA
; ORGANISM: mouse
US-09-940-727B-105

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Query Match 61.7%; Score 253.4; DB 11; Length 366;  
Best Local Similarity 84.0%; Pred. NO. 9.8e-75;  
Matches 300; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 55  | GATGTGCAGCTTCAAGAGTCGGGACCTGTCTCTGGTGAAGCCCTTCTCAGTCTCTGTCCCTC | 114 |
| Db | 1   | GACGTGCAGTTGCGAGGATCGGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCCTC     | 60  |
| Qy | 115 | ACCTGCACCTGTCACTGGCTACTCAATCACCAGTGATCATGCTCGAGCTGGATCGGCAG    | 174 |
| Db | 61  | ACCTGCACCTGTCACTGGCAATTCAATCACCAGTGATTATGCTCGACTGGATCGGCAG     | 120 |
| Qy | 175 | TTTCCAGGAAACAACCTCGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTAC    | 234 |
| Db | 121 | TTTCCAGGAAACAACCTCGAGTGGATGGGTACATAAAGGCACATTTATGGCACTAGGTAC   | 180 |
| Qy | 235 | AACCCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACAGATTCTTC    | 294 |
| Db | 181 | AACCCCTTCTCATTAAGTCGAACTCTATCACTCGAGACACGTCCAAGAACAGATTCTTC    | 240 |
| Qy | 295 | CTACAGTTGAAATTCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATCCCTA   | 354 |
| Db | 241 | CTGCAGTTGGATTCTGTGACTGCTGAGGACACAGCCACATATTTATGTGAAGATATCAT    | 300 |
| Qy | 355 | GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACTCAGTCAACCGTCTCTCTCA     | 411 |
| Db | 301 | TACTACGGTTCGGCT-----TACTGGGSCCAAGGACTCTGGTCACTGTCTCTGCA        | 351 |

## RESULT 15

RES001 13  
US-09-940-727B-109  
; Sequence 109, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095

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1  PRIOR FILING DATE: 1998-12-28
2  PRIOR APPLICATION NUMBER: PCT/US97/10965
3  PRIOR FILING DATE: 1997-06-25
4  PRIOR APPLICATION NUMBER: 08/672,345
5  PRIOR FILING DATE: 1996-06-25
6  NUMBER OF SEQ ID NOS: 121
7  SOFTWARE: PatentIn version 3.1
8  SEQ ID NO 109
9  LENGTH: 420
10 TYPE: DNA
11 ORGANISM: mouse
12 FEATURE:
13 NAME/KEY: misc_feature
14 LOCATION: (21)..(21)
15 OTHER INFORMATION: any nucleotide
16 FEATURE:
17 NAME/KEY: misc_feature
18 LOCATION: (28)..(28)
19 OTHER INFORMATION: any nucleotide
20 FEATURE:
21 NAME/KEY: misc_feature
22 LOCATION: (31)..(31)
23 OTHER INFORMATION: any nucleotide
24 FEATURE:
25 NAME/KEY: misc_feature
26 LOCATION: (37)..(37)
27 OTHER INFORMATION: any nucleotide
28 FEATURE:
29 NAME/KEY: misc_feature
30 LOCATION: (40)..(40)
31 OTHER INFORMATION: any nucleotide
32 FEATURE:
33 NAME/KEY: misc_feature
34 LOCATION: (49)..(49)
35 OTHER INFORMATION: any nucleotide
36 FEATURE:
37 NAME/KEY: misc_feature
38 LOCATION: (56)..(56)
39 OTHER INFORMATION: any nucleotide
40 US-09-940-727B-109

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Query Match 59.8%; Score 245.6; DB 11; Length 420;  
Best Local Similarity 87.4%; Pred. No. 4.3e-72;  
Matches 292; Conservative 0; Mismatches 36; Indels 6; Gaps 2;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 70  | GAATCGGGACCTGTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACTGCACTGTCACT   | 129 |
| Db | 47  | GANAGGGGGNCGGAGCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACTGCACTGTCACT    | 106 |
| Qy | 130 | GGCTACTCAATACCACTGATCATGCCTCTGGAGCTGGATCCGGCAGTTCCTCAGGAACAACA | 189 |
| Db | 107 | GGCTACTCAATACCACTGATTAATGCTCGGAACCTGGATCCGGCAGTTCCTCAGGAACAACA | 166 |
| Qy | 190 | CTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACTACAACCCACTCTCTCAAA    | 249 |
| Db | 167 | CTGGAGTGGATGGGCTACATAAGGTACAGTGGTATCACTAGGTACAACCCACTCTCTCAAA  | 226 |
| Qy | 250 | AGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTTCTTCTCCTACAGTTGAATCT | 309 |
| Db | 227 | AGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTTCTTCTCCTCAGTTAAATCT  | 286 |
| Qy | 310 | GTGACTACTGGGGACAGTCCACATATTTACTGTGCAAGATCCCTAGCTCGGACTACGGCT   | 369 |
| Db | 287 | GTGACTACTGAGGACACAGCCACTTATTACTGTGTAAGA-----ATTCACTACTACGGCT   | 341 |
| Qy | 370 | ATGACTACTGGGGTCAAGGAACCTCAGTCAACG                              | 403 |
| Db | 342 | ACGG-CAACTGGGGCAAGGCACCACTCTCAAG                               | 374 |

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Job time : 977.625 secs

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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:51:21 ; Search time 58.1212 Seconds  
(without alignments)  
3121.209 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATGAGAGTGTGATTCTTTT.....CCTCAGTCACCGTCTCCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 411   | 100.0       | 411    | 1  | US-08-137-117D-30  |
| 2          | 411   | 100.0       | 411    | 1  | US-08-436-717-30   |
| 3          | 297.8 | 72.5        | 357    | 3  | US-08-767-128-17   |
| 4          | 284.6 | 69.2        | 836    | 2  | US-08-933-616-1    |
| 5          | 284.6 | 69.2        | 836    | 3  | US-08-279-307-1    |
| 6          | 284.6 | 69.2        | 836    | 4  | US-09-135-121B-3   |
| 7          | 277.6 | 67.5        | 720    | 2  | US-07-956-399-1    |
| 8          | 264.4 | 64.3        | 354    | 3  | US-09-065-059-12   |
| 9          | 260   | 63.3        | 639    | 4  | US-09-170-769A-1   |
| 10         | 258.2 | 62.8        | 366    | 2  | US-08-672-345C-87  |
| 11         | 258.2 | 62.8        | 366    | 3  | US-09-214-095D-101 |
| 12         | 255.8 | 62.2        | 426    | 3  | US-08-554-840-28   |
| 13         | 255.8 | 62.2        | 426    | 4  | US-08-925-339-28   |
| 14         | 255.8 | 62.2        | 426    | 4  | US-09-332-595-28   |
| 15         | 253.4 | 61.7        | 366    | 2  | US-08-672-345C-89  |
| 16         | 253.4 | 61.7        | 366    | 3  | US-09-214-095D-105 |
| 17         | 250.2 | 60.9        | 351    | 2  | US-08-308-494A-14  |
| 18         | 245.6 | 59.8        | 420    | 3  | US-09-214-095D-109 |
| 19         | 245.4 | 59.7        | 419    | 3  | US-09-214-095D-113 |
| 20         | 244   | 59.4        | 830    | 1  | US-08-133-011-115  |
| 21         | 244   | 59.4        | 830    | 1  | US-08-322-730A-115 |
| 22         | 244   | 59.4        | 830    | 1  | US-08-387-874-88   |
| 23         | 244   | 59.4        | 830    | 2  | US-08-383-619-115  |
| 24         | 244   | 59.4        | 830    | 3  | US-08-907-739-115  |
| 25         | 244   | 59.4        | 830    | 4  | US-09-729-597-115  |
| 26         | 244   | 59.4        | 830    | 5  | PCT-US93-08364-88  |
| 27         | 243.4 | 59.2        | 2010   | 3  | US-09-070-637-19   |

Sequence 99, Appl  
Sequence 99, Appl  
Sequence 71, Appl  
Sequence 99, Appl  
Sequence 99, Appl  
Sequence 99, Appl  
Sequence 71, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 14, Appl  
Sequence 68, Appl  
Sequence 68, Appl  
Sequence 3, Appl  
Sequence 62, Appl  
Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-137-117D-30  
; Sequence 30, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 411 base pairs  
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..411
US-08-137-117D-30

Query Match      100.0%; Score 411; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.6e-132;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTCTGATCTTTTGGGTGTTTCACAGCCTTTCCTGGTATCCTGTCATGTCG 60
DB 1 ATGAGAGTCTGATCTTTTGGGTGTTTCACAGCCTTTCCTGGTATCCTGTCATGTCG 60

QY 61 CAGCTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB 61 CAGCTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120

QY 121 ACTGTCAGTGGTACTCAATCAACAGTATCATGCTGGAGCTGGATCGGCGAGTTTCCA 180
DB 121 ACTGTCAGTGGTACTCAATCAACAGTATCATGCTGGAGCTGGATCGGCGAGTTTCCA 180

QY 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACAACCCA 240
DB 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACAACCCA 240

QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCCAGTTCTTCTACAG 300
DB 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCCAGTTCTTCTACAG 300

QY 301 TTGAATTTCTGACTACTGGGACACCGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
DB 301 TTGAATTTCTGACTACTGGGACACCGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360

QY 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411

RESULT 2
US-08-436-717-30
; Sequence 30, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
```

APPLICANT: GOEBEL, PETER  
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
NUCLEOTIDES CODING THEREFORE  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 611079west Center, 90 South Seventh St  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,128  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09258  
FILING DATE: 05-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/541,373  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.49USF1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/371-5278  
TELEFAX: 612/332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...357  
OTHER INFORMATION:  
US-08-767-128-17

Query Match 72.5%; Score 297.8; DB 3; Length 357;  
Best Local Similarity 89.6%; Pred. No. 5.6e-93;  
Matches 320; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
Qy 55 GATGTGACGCTCAGGAGTCGGGACCTCTCGTGGTGAAGCCCTCTCAGTCTCTCCCTC 114  
Db 1 GATGTGACGCTCAGGAGTCGGGACCTCTCGTGGTGAAGCCCTCTCAGTCTCTCCCTC 60  
Qy 115 ACCTGCACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGTGGATCGGCGAG 174  
Db 61 ACCTGCACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGTGGATCGGCGAG 120  
Qy 175 TTTCAGGAAACAACTGAGTGGATGGGCTACATAAGTTACAGTGGATCAGTACCTAC 234  
Db 121 TTTCAGGAAACAACTGAGTGGATGGGCTACATAAGTACAGTGGATGAGTACCTAGCTAC 180

Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCAAGTCTTC 294  
Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCAAGTCTTC 240  
Qy 295 CTACAGTTGAATCTGTGACTACTGGGACACGCTCCACATATTACTGTGAAGATCCCTA 354  
Db 241 CTGAGTTGAATCTGTGACTACTGGGACACGCTCCACATATTACTGTGAAGATGGGT 300  
Qy 355 GCTCGGACTACGGCTATGAGTACTTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 301 AACTACCCGTGGTACTTTGACTACTGGGGCAAGGACCACTCTCACAGTCTCTCTCA 357  
RESULT 4  
US-08-933-616-1  
Sequence 1, Application US/08933616  
Patent No. 5869331  
GENERAL INFORMATION:  
APPLICANT: Dornburg, Ralph C.  
TITLE OF INVENTION: Cell-Type Specific Gene Transfer Using  
Retroviral Vectors Containing Antibody-Envelope Fusion  
TITLE OF INVENTION: Proteins and Wild-Type Envelope Fusion Proteins  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard R. Muccino  
STREET: P. O. Box 1267  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08551  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,616  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,980  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Muccino, Richard R.  
REGISTRATION NUMBER: 32,538  
REFERENCE/DOCKET NUMBER: UMD1-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 466-3407  
TELEFAX: (609) 466-2760  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 836 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-933-616-1  
Query Match 69.2%; Score 284.6; DB 2; Length 836;  
Best Local Similarity 84.2%; Pred. No. 3.1e-88;  
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;  
Qy 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTACAGCCCTTCTGGTATCTGTCTGTGATGTG 60  
Db 43 ATGAGTGTGTAAGTCTTCTGTACCTTGTGACAGCCCTTCGGGTATCTGTCTAGAGGTG 102  
Qy 61 CAGCTTCAGGAGTCGGGACCTGCTCGTGAAGCTTCTCAGTCTGTGCTCCCTCACCTGC 120  
Db 103 CAGCTTCAGGAGTCAGGACCTAGCTCTGTAACCTTCTGTGACTCTGTCCCTCACCTGT 162  
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGTGGATCCGCGCAGTTTCCA 180

Db 163 TCTGTCACTGGGACTCCATCACCAGTGGTTA---CTGGAACCTGGATCCGGAATATCCCA 219  
QY 181 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCA 240  
Db 220 GGAATAAACTTGAGTACATGGGTACATAAGCTACAGTGGTAGCATTACTACCAATCCA 279  
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACAGTTCTTCTCTACAG 300  
Db 280 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACAGTTACTACCTGCAG 339  
QY 301 TTGAATTTGTGACTACTGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
Db 340 TTGAATTTGTGACTACTGGGACAGTCCACATATTACTGTGCAAGAT---ATGGTGGT 396  
QY 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411  
Db 397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 447

## RESULT 5

US-08-279-307-1  
; Sequence 1, Application US/08279307  
; Patent No. 6146885  
; GENERAL INFORMATION:  
; APPLICANT: Dornburg, Ralph C.  
; TITLE OF INVENTION: Cell-Type Specific Gene Transfer  
; TITLE OF INVENTION: Using Retroviral Vectors Containing Antibody-Envelope  
; TITLE OF INVENTION: Fusion Proteins  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard R. Muccino  
; STREET: P.O. Box 1267  
; CITY: Princeton  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08551  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/279,307  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/07/979,619  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muccino, Richard R.  
; REGISTRATION NUMBER: 32,538  
; REFERENCE/DOCKET NUMBER: UM01-016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 466-3407  
; TELEFAX: (609) 466-2760  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 836 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-279-307-1  
Query Match 69.2%; Score 284.6; DB 3; Length 836;  
Best Local Similarity 84.2%; Pred. No. 3.1e-88;  
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;

QY 1 ATGAGAGTCTGATCTTTTGTGGCTTTTCACAGCCTTTCCTGGTATCTCTGTCTGATGTG 60  
Db 43 ATGATGGTGTAACTTCTCTGTACCTGTTGACAGGCCCTTCCGGGTATCTCTGTCTGATGTG 102

QY 61 CAGCTTCAGGAGTCGGGACCTGTCTCTGTGAAGCTTTCTCAGTCTCTGTCTCTCACCTGC 120  
Db 103 CAGCTTCAGGAGTCAGGACCTAGCTCGTGAACCTTCTCTGACTCTGTCTCTCACCTGT 162  
QY 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGAGGTTTCCA 180  
Db 163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACCTGGATCCGGAATATCCCA 219  
QY 181 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCA 240  
Db 220 GGAATAAACTTGAGTACATGGGTACATAAGCTACAGTGGTAGCATTACTACCAATCCA 279  
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACAGTTCTTCTCTACAG 300  
Db 280 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACAGTTACTACTCTGAG 339  
QY 301 TTGAATTTGTGACTACTGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
Db 340 TTGAATTTGTGACTACTGGGACAGTCCACATATTACTGTGCAAGAT---ATGGTGGT 396  
QY 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411  
Db 397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 447

## RESULT 6

US-09-135-121B-3  
; Sequence 3, Application US/09135121B  
; Patent No. 6534051  
; GENERAL INFORMATION:  
; APPLICANT: Dornburg, Ralph C.  
; TITLE OF INVENTION: CELL-TYPE SPECIFIC GENE TRANSFER USING RETROVIRAL VECTORS  
; TITLE OF INVENTION: CONTAINING ANTIBODY-ENVELOPE FUSION PROTEINS AND WILD-TYPE  
; FILE REFERENCE: 97,216-L  
; CURRENT APPLICATION NUMBER: US/09/135,121B  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: US 08/933,616  
; PRIOR FILING DATE: 1997-08-28  
; PRIOR APPLICATION NUMBER: US 08/205,980  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 07/979,619  
; PRIOR FILING DATE: 1992-11-20  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Microsoft Word 97  
; SEQ ID NO 3  
; LENGTH: 836  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: B6.2 gene encoding single chain antibody against hapten DNP  
US-09-135-121B-3

Query Match 69.2%; Score 284.6; DB 4; Length 836;  
Best Local Similarity 84.2%; Pred. No. 3.1e-88;  
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;

QY 1 ATGAGAGTCTGATCTTTTGTGGCTTTTCACAGCCTTTCCTGGTATCTCTGTCTGATGTG 60  
Db 43 ATGATGGTGTAACTTCTCTGTACCTGTTGACAGGCCCTTCCGGGTATCTCTGTCTGAGAGTG 102  
QY 61 CAGCTTCAGGAGTCGGGACCTGTCTCTGTGAAGCTTCTCAGTCTCTGTCTCTCACCTGC 120  
Db 103 CAGCTTCAGGAGTCAGGACCTAGCTCGTGAACCTTCTCTGACTCTGTCTCTCACCTGT 162  
QY 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGAGGTTTCCA 180  
Db 163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACCTGGATCCGGAATATCCCA 219  
QY 181 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCA 240  
Db 220 GGAATAAACTTGAGTACATGGGTACATAAGCTACAGTGGTAGCATTACTACCAATCCA 279

Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCGAGTCTTCTCTACAG 300  
Db 280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAAGAACCGAGTCTCTCGAG 339  
Qy 301 TTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
Db 340 TTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGAT---ATGGTGGT 396  
Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 447

## RESULT 7

US-07-956-399-1  
; Sequence 1, Application US/07956399  
; Patent No. 5876717  
; GENERAL INFORMATION:  
; APPLICANT: SHIMAMURA, TOSHIRO  
; APPLICANT: TAKI, SHINGSUKE  
; APPLICANT: HAMURO, JUNJI  
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY  
; TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/956.399  
; FILING DATE: 19921005  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5876717man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 10-586-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 720 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..720  
US-07-956-399-1

Query Match 67.5%; Score 277.6; DB 2; Length 720;  
Best Local Similarity 88.2%; Pred. No. 7.4e-86;  
Matches 314; Conservative 0; Mismatches 39; Indels 3; Gaps 1;  
Qy 56 ATGTGACGTTTCAGGAGTCGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTCA 115  
Db 368 AGGTCAACTCGAGGAGTCTGGACCTGGCGCTGGTGAACCTTCTCAGTCTCTGTCCTCA 427  
Qy 116 CTGACGTCGCTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCGGGAGT 175  
Db 428 CTGACGTCGCTGGCTACCCCAATCACCAGTGATTTATGCTGGAGCTGGATCGGGAGT 487

Qy 176 TTCAGAGAAACAACTGGAGTGAATGGGCTACATAAGTTACAGTGGTATCACTACCTACA 235  
Db 488 TTCAGAGAAACAACTGGAGTGAATGGGCTACGTAAGCTACAGTGGTATGACCTACCTACA 547  
Qy 236 ACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCGATTCCTCC 295  
Db 548 ACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCGATTCCTCC 607  
Qy 296 TACAGTTGAATTTCTGTGACTACTGGGACACAGTCCACATATTACTGTGCAAGATCCCTAG 355  
Db 608 TGCAGTTGAATTTCTGTGACTACTGGGACACAGTCCACATATTACTGTGCAAGA---GGTG 664  
Qy 356 CTCGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 665 GTTCCCTATGCTATGGACTACTGGGGTCAAGGGACCGGTCAACCGTCTCTCTCA 720

## RESULT 8

US-09-065-059-12  
; Sequence 12, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAYAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,059  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: P-42,368  
; REFERENCE/DOCKET NUMBER: 50356-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-518-5100  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 354 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna to mRNA  
US-09-065-059-12

Query Match 64.3%; Score 264.4; DB 3; Length 354;  
Best Local Similarity 84.2%; Pred. No. 1.8e-81;  
Matches 298; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
Qy 58 GTGAGCTTCAGGAGTCGGACCTGCTCGTGGTGAAGCCTTCTCAGTCTCTGTCCTCACC 117  
Db 1 GTGAGCTGCAGGAGTCTGGACCTGGCCCTCGTGAACCTTCTCAGTCTCTGTCCTCACC 60  
Qy 118 TGCAGTCTGCTACTGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGCGAGTTT 177  
Db 61 TGCTCTGCTACTGGCTACTCCATCACCAGTGGTATTACTTACTGGAACTGGATCCGCGAGTTT 120

QY 178 CCAGGAAACAACTGGAGTGGCTACATAGTTACAGTGGTATCAGTACCTACCAAC 237  
Db 121 CCAGGAAACAACTGGAGTGGCTACATAGTTACAGTGGTATCAGTACCTACCAAC 180  
QY 238 CCATCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCAAGAACAGGTTCTTCTTA 297  
Db 181 CCATCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCAAGAACAGGTTCTTCTTA 240  
QY 298 CAGTTGAAATTCGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCT 357  
Db 241 AAGTTGAAATTCGTGACTACTGGGACAGCTCCACATATTACTGTGCGGTTTATTACTAC 300  
QY 358 CGGACTACGGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 301 GATGGTAGTCTTTTGACTACTGGGCGCAAGGACACCGTCACCGTCTCTCTCA 354

RESULT 9  
US-09-170-769A-1  
; Sequence 1, Application US/09170769A  
; Patent No. 6444206  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: LETURCO, Didier  
; APPLICANT: MORIATRY, Ann  
; APPLICANT: ULEVITCH, Richard  
; APPLICANT: TOBIAS, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA  
; FILE REFERENCE: SCRIPT140-3  
; CURRENT APPLICATION NUMBER: US/09/170,769A  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: US 08/070,160  
; PRIOR FILING DATE: 1993-05-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 639  
; TYPE: DNA  
; ORGANISM: Murine  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(639)  
US-09-170-769A-1

Query Match 63.3%; Score 260; DB 4; Length 639;  
Best Local Similarity 93.2%; Pred. No. 8.2e-80; Mismatches 20; Indels 0; Gaps 0;  
Matches 272; Conservative 0;  
QY 62 AGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGCA 121  
Db 11 AGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCCTCACCTGCA 70  
QY 122 CTGTCACTGGCTACTGAATACAGTATCATGCTGGAGTGGATCCGGGAGTTTCCAG 181  
Db 71 CTGTCACTGGCTACTCAATCAGCAGTATCTGCTGGAACCTGGATCCGGGAGTTTCCAG 130  
QY 182 GAAACAACTGGAGTGGGCTACATAGTTACAGTGGTATCACTACTACACCCAT 241  
Db 131 GAAACAGACTGGAGTGGGCTACATAGTTACAGTGGTATCACTACTACACCCAT 190  
QY 242 CTCTCAAAAGTCCGATCTCTATCACTCGAGACACATCCAAAGAACAGTCTTCTCTACAGT 301  
Db 191 CTCTCAAAAGTCCGATCTCTATCACTCGAGACACATCCAAAGAACAGTCTTCTCTGAGT 250  
QY 302 TGAATTCGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCT 353  
Db 251 TGAATTCGTGACTACTGAGGACACAGCCACATATTACTGTGTAAGAGGGCT 302

RESULT 10  
US-08-672-345C-87  
; Sequence 87, Application US/08672345C  
; Patent No. 5948658

; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-672-345C-87

Query Match 62.8%; Score 258.2; DB 2; Length 366;  
Best Local Similarity 84.9%; Pred. No. 2.6e-79;  
Matches 303; Conservative 0; Mismatches 48; Indels 6; Gaps 1;  
QY 55 GATGTGCAGCTTCAGGAGTCGGGACCTGCTCTGTGTGAAGCCTTCTCAGTCTCTGTCCCTC 114  
Db 1 GATGTGCAGCTTCAGGAGTCGGGACCTGCGCTGTGTAACCTTCTCAGTCTCTGTCCCTC 60  
QY 115 ACCTGCAGCTGCTACTGGCTACTCAATCACCAGTGCATCATGCTGGAGTGGATCCGGCAG 174  
Db 61 ACCTGCAGCTGCTACTGGCAATTCATCACCAGTGCATCATGCTGGAGTGGATCCGGCAG 120  
QY 175 TTTCAGGAAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCAGTACCTTAC 234  
Db 121 TTTCAGGAAACAACTGGAGTGGGCTACATAAGGCACATTTATGGCAGTAGGTAC 180  
QY 235 AACCCATCTCTCAAAAGTCCGAATCTCTATCACTCGAGACACATCCAAAGAACAGTCTTCTC 294  
Db 181 AACCCCTTCTCTATAAGTCCGAATCTCTATCACTCGAGACAGCTCCAAAGAACAGTCTTCTC 240  
QY 295 CTACAGTTGATTTCTGTGACTACTGGGACACAGTCCACATATTACTGTGCAAGATCCCTCA 354  
Db 241 CTGAGTTGGATTTCTGTGACTGCTGAGGACACAGCCACATATTATTGTGAAGATATCAT 300  
QY 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 301 TACTACGGTTCCGGCT-----TACTGGGGCAAGGACTCTGGTCTCTCTGCA 351

RESULT 11  
US-09-214-095D-101  
; Sequence 101, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US

```
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-101

Query Match      62.8%; Score 258.2; DB 3; Length 366;
Best Local Similarity 84.9%; Pred. No. 2.6e-79;
Matches 303; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 114
Db 1 GATGTCAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 60

Qy 115 ACCTGCACTGTCAGTGGTCTCAATCAACAGTGATCATGCTGGAGCTGGATCCGGCAG 174
Db 61 ACCTGCACTGTCAGTGGCAATTCATCAACAGTGATCATGCTGGAGCTGGATCCGGCAG 120

Qy 175 TTTCCAGAAACAACCTGAGTGGCTACATAGTATGATGATGATGATGATGATGATGAT 234
Db 121 TTTCCAGAAACAACCTGAGTGGCTACATAGTATGATGATGATGATGATGATGATGAT 180

Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCTGCTTC 294
Db 181 AACCTTCTCTCATAGTCGAATCTCTATCACTCGAGACAGTCCAAAGAACCTGCTTC 240

Qy 295 CTACAGTTGAATCTGTGACTACTGGGACACAGTCCACATATTAATGTCGAAGATCCCTA 354
Db 241 CTGCAAGTTGAATCTGTGACTGCTGAGACACAGCCACATATTATTGTAAGATATCAT 300

Qy 355 GCTCGGACTACGGCTATGCACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCA 411
Db 301 TACTACGGTTCGGT-----TACTGGGGCCAAAGGACTCTGGTCACTGCTCTGCA 351

RESULT 12
US-08-554-840-28
; Sequence 28, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..426
US-08-554-840-28

Query Match      62.2%; Score 255.8; DB 3; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.9e-78;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

Qy 1 ATGAGAGTGTGATCTTTTGTGGTGTTCACAGCCTTCTCGTATCTCTGTCATCTGTGATGTG 60
Db 7 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCCGGGTTTCTCTGTCAAGAGTG 66

Qy 61 CAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
Db 67 CAGCTTCAGGAGTCAGGACCTAGCTCTGTAACCTTCTCAGACTCTGCTCCCTCACCTGT 126

Qy 121 ACTGTCACTGGCTACTCAATCACAGTGATCATGCTCGAGCTGGATCCGGCAGTTTCCA 180
Db 127 TCTGTCACTGGCAGCTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAATTTCCA 183

Qy 181 GGAACAACCTGGAGTGGGTACATAAGTTTACAGTGTATCATCTACTACAAACCCA 240
Db 184 GGAATAAACCTTGAGTACATGGGCTACATAAGTTTACAGTGTATCATCTACTACAAACCA 243

Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCCAAGAACCTGTTCTTCTCTACAG 300
Db 244 TCTCTCAAGAGTCGAATCTCTCACTCGGACACATCCCAAGAACCTGTTCTACTACAA 303

Qy 301 TTGAATTTCTGTGACTACTGGGACACGTCACACATATTACTGTGCAAGATCCCTAGCTCGG 360
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RESULT 13
US-08-925-339-28
; Sequence 28, Application US/08925339
; Patent No. 6440418
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; TELEPHONE:
```

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE: 07-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 7..426  
US-08-925-339-28

Query Match 62.2%; Score 255.8; DB 4; Length 426;  
Best Local Similarity 79.4%; Pred. No. 1.9e-78;  
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;  
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RESULT 14  
US-09-332-595-28  
Sequence 28, Application US/09332595  
Patent No. 6506383  
GENERAL INFORMATION:  
APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia

COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/332,595  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 7..426  
US-09-332-595-28

Query Match 62.2%; Score 255.8; DB 4; Length 426;  
Best Local Similarity 79.4%; Pred. No. 1.9e-78;  
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;  
QY 1 ATGAGAGTGTGATCTTTTGTGGCTGTTCACAGCCTTCTCGGTATCTGTCTGATGTG 60  
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DB 244 TCTCTCAAGAGTCGAATCTCCATCACTCGGACACATCCAGAACCTGCTTCTACCTCAA 303  
QY 301 TTGAATTTCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
DB 304 TTGAATTTCTGTGACTACTGGGACACGTCACATATTACTGTGCTGCTGCGGAGTTACGGG 363  
QY 361 ACTAGCGC-----TATGGACTACTGGGTCAGGAACCTCAGTCACCGTCTCTCTCA 411  
DB 364 AGGACCCGCTACTACTTTGACTTCTGGGCGCAAGGCACCACTCTCAGCGTCTCTCTCA 420

RESULT 15  
US-08-672-345C-89  
Sequence 89, Application US/08672345C  
Patent No. 594858  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY



NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-672-345C-89

Query Match 61.7%; Score 253.4; DB 2; Length 366;  
Best Local Similarity 84.0%; Pred. No. 1.2e-77;  
Matches 300; Conservative 0; Mismatches 51; Indels 6; Gaps 1;  
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Db 241 CTGCAAGTTGGATTCTGTGACTGCTGAGGACACAGCCACATATTATTGTGAAGATATCAT 300  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 411  
Sequence: 1 ATGAGAGTGCTGATCTTTT.....CCTCAGTCACGGTCTCCTCA 411

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum:\*  
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7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
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11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
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23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
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27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 39 | 193.8 | 47.2 | 677  | 10 | BG686767 | BG686767  |
| 40 | 192.6 | 46.9 | 959  | 13 | BQ899307 | BQ899307  |
| 41 | 192.2 | 46.8 | 1050 | 9  | AL552672 | AL552672  |
| 42 | 191.8 | 46.7 | 935  | 13 | BQ710683 | BQ710683  |
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ALIGNMENTS

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693 bp mRNA  
mRNA sequence.  
ACCESSION BI456288  
VERSION BI456288.1 GI:15246944  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 693)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM1636 row: 1 column: 20  
High quality sequence stop: 691.

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Best Local Similarity 92.3%; Pred. No. 4.5e-89;
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ACCESSION BU524092
VERSION BU524092.1 GI:22834531
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 963)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM14133 row: d column: 16
High quality sequence stop: 420.
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/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
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ORIGIN
Query Match 83.2%; Score 342; DB 13; Length 963;
Best Local Similarity 90.8%; Pred. No. 6e-89;
Matches 376; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCCTGTCGTGATGG 60
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QY 121 ACTGTCACTGCTACTCAATCACCAGTATCATCGCTGGAGCTGGATCCGCGAGTTTCCA 180
DB |||||||
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DB |||||||
DB 327 TTGAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATATGAGGTAAC 386
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DB |||||||
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LOCUS BU007948 RIKEN full-length enriched, B cells CRL-1702 WEHI 231 cDNA
DEFINITION Mus musculus cDNA clone G4D0003J12 5', mRNA sequence.
ACCESSION BU007948
VERSION BU007948.1 GI:26068197
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamada, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
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Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

**TITLE**  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

**JOURNAL**  
Nature 420, 563-573 (2002)

**MEDLINE**  
22354683

**PUBMED**  
1246851

**COMMENT**  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp  
URL: <http://genome.gsc.riken.go.jp/>  
Arakawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details..

**FEATURES**  
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Best Local Similarity 89.5%; Pred. No. 1.6e-85;  
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DB 243 GGAACAACAACTGGAGTGGTGGCTACATAAGTTTACAGTGGTATCACTACTACCTCAACACCCA 302  
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## RESULT 4

BG962947

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-i@mail.nih.gov](mailto:cgabs-i@mail.nih.gov)

Tissue Procurement: Jeffrey B. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLAM10986 row: 0 column: 07

High quality sequence stop: 658.

Location/Qualifiers

1. 659

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/db\_xref="taxon:10090"

/clone="IMAGE:4983006"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI;

Site2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

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Matches 370; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

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DEFINITION 602834949F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989229 5',
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ACCESSION  BG969011
VERSION     BG969011.1 GI:14356648
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
AUTHORS     Contact: Robert Strausberg, Ph.D.
            Email: cgabs@mail.nih.gov
            Tissue procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11003 row: b column: 14
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                /lab_host="DH10B (T1 phage-resistant)"
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                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT."

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Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Matches 365; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

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DEFINITION  BB859416 RIKEN full-length enriched, B cells CRL-1702 WEHI 231 CDNA
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ACCESSION  BB859416
VERSION     BB859416.1 GI:17100870
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 483)
AUTHORS     Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
            Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
            , Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
            Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
            , Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
            Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
            , A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
            Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
            2001)
            Unpublished
CONTACT: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
```

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi.K., Fujiwaka.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E., Watahiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsuura.S., Kawai.J., Okazaki.Y., Muramatsu.M., Inoue.Y., Kira.A. and Hayashizaki.Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Konno.H., Fukunishi.Y., Shibata.K., Itoh.M., Carninci.P., Sugahara.Y. and Hayashizaki.Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

#### FEATURES

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 VERSION B1249884.1 GI:14797694  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 909)  
 NIH-MGC <http://mgc.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM11375 Row: m Column: 21  
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#### FEATURES

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BASE COUNT 207 a 255 c 224 g 223 t

#### Query Match

Best Local Similarity 78.2%; Score 321.2; DB 12; Length 909;  
 Matches 363; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

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#### RESULT 8

BQ922384

#### LOCUS

853 bp mRNA linear EST 20-AUG-2002

BQ922384

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IMAGE:6477196 5', mRNA sequence.
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VERSION     BQ922384.1
KEYWORDS    BQ922384.1 GI:22337415
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 853)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Cloning Distribution: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14018 row: m column: 05
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                /note="Organ: Colon; Vector: pCMV-SPORT6; Site: 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI CGAP Library."
BASE COUNT  194 a 242 c 196 g 205 t
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Query Match      76.1%; Score 312.8; DB 13; Length 853;
Best Local Similarity 93.7%; Pred. No. 2e-80;
Matches 326; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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RESULT 9
BF582341
LOCUS      602101173F1 NCI_CGAP_Co24 910 bp mRNA linear EST 12-DEC-2000
DEFINITION 602101173F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:422483 5',
mRNA sequence.
ACCESSION   BF582341
VERSION     BF582341.1
KEYWORDS    BF582341.1 GI:11656053
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 910)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Cloning Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9814 row: a column: 20
            High quality sequence stop: 669.
            Location/Qualifiers
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                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:422483"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NCI CGAP Co24"
                /note="Organ: Colon; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI CGAP Library."
BASE COUNT  193 a 239 c 254 g 224 t
ORIGIN
Query Match      76.1%; Score 312.6; DB 10; Length 910;
Best Local Similarity 86.6%; Pred. No. 2.3e-84;
Matches 356; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
QY 1 ATGAGAGTCTCATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCATGTG 60
DB 33 ATGAGAGTCTCATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCATGTG 91
QY 61 CAGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB 92 CCGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCGTCACCTGC 151
QY 121 ACTGTCACTGGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCGGACGAGTTTCCA 180
DB 152 ACTGTCACTGGCTACTCCTTCCACAGTGGTTATTACTGGAACTGGATCGGACGAGTTTCCA 211
QY 181 GGAACAAACTCGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTACAAACCCA 240
DB 212 GGAACAAACTCGAGTGGATGGCTACATACTCAACAGTGGTAGTACTAAGTACAAACCCA 271
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTTCTTCTACAG 300
DB 272 TTTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTTCTTCTGAG 331
QY 301 TTGAATTTCTGTACTACTGGGACACAGCTCCACATATTACTGTGCAAGATCCTAGTCCG 360
DB 332 TTGAATTTCTGTACTACTGAGGACACAGCCACATATTACTGTGAGGGGAATAGTTAAC 391
QY 361 ACTACGGCTATGAGTACTTGGGGTCAAGAAACCTCAGTCACCGTCTCTCA 411
DB 392 CTGTACTACTTTGACTACTGGGGCAAGGCCACCACCTCTCACAGTCTCGTCA 442
RESULT 10
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BI249876 853 bp mRNA linear EST 17-JUL-2001  
 LOCUS 60295978F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5151882 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI249876  
 VERSION BI249876.1 GI:14797680  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 853)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)  
 AUTHORS Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11375 row: k column: 19  
 High quality sequence stop: 799.  
 Location/Qualifiers  
 1..853  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5151882"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP Mam5"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

BASE COUNT 208 a 232 c 200 g 213 t  
 ORIGIN  
 Query Match 75.6%; Score 310.6; DB 12; Length 853;  
 Best Local Similarity 87.2%; Pred. No. 8.7e-80; Mismatches 44; Indels 10; Gaps 2;  
 Matches 367; Conservative 0;

QY 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGC-CTTTCCTGGTATCCTCTGTGATGT 59  
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 DB 25 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCGCTTCTCGTTCTGTCTAATGT 84  
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 QY 60 GCAGTTTCAGAGTCGGGACCTGCTCTGGTGAAGCTTCTCAGTCTCTGTCCCTCAGCTG 119  
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 DB 85 GCAGTTTCAGAGTCAGGACCTGGGCTGGTGAAGCTTCTCAGTCTCTGTCTGTCACCTG 144  
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 QY 120 CACTGTCACTGGCTACTCAATCACAGTGATCATCCCTGGAGCTGGATCCGGCAGTTTCC 179  
 |||||  
 DB 145 CACTGTCACTGGCTACTCCATCACAGTACTTATAGCTGGAACTGGATCCGGCAGTTTCC 204  
 |||||  
 QY 180 AGGAAACAAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 239  
 |||||  
 DB 205 AGGAAACAAACTGGAGTGGGCTACATACACTACAGTGGTACATAATTAACACCC 264  
 |||||  
 QY 240 ATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTTACA 299  
 |||||  
 DB 265 ATCTCTAAAAGTCGAGTCTCTATTACTCGAGACACATCCAAAGAACCAAGTTCTTCTTCCA 324  
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 QY 300 GTTGAATCTGTGACTACTGGGACACGTCCACATATTACTGTGCAAGA-----TC 350  
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 DB 325 GTTGAATCTGTGACTACTGGGACACAGCCACATATTACTGTGCAAGAGGGGACTTACTA 384  
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QY 351 CCTAGCTCGGACTACGGCTATGACTACTGGGTCAAGGAACCTCAGTCAACCGTCTCCTC 410  
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 DB 385 TAGTTACATCCCTATGCTTTGGACTATTGGGTCAAGGAACCTCAGTCAACCGTCTCCTC 444  
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 QY 411 A 411  
 DB 445 A 445  
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RESULT 11  
 LOCUS BF578272  
 DEFINITION 602092608F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4207320 5',  
 mRNA sequence.  
 ACCESSION BF578272  
 VERSION BF578272.1 GI:11651984  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 933)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)  
 AUTHORS Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM9769 row: o column: 01  
 High quality sequence stop: 655.  
 Location/Qualifiers  
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 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4207320"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI\_CGAP Co24"  
 /note="Organ: Colon; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 235 a 261 c 245 g 192 t  
 ORIGIN  
 Query Match 71.3%; Score 293; DB 10; Length 933;  
 Best Local Similarity 93.7%; Pred. No. 1.3e-74;  
 Matches 327; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

QY 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCTTCTCGTATCTCTGTGATGTG 60  
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 DB 54 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCTTCTCGTATCTCTGTGATGTG 112  
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 QY 61 CAGCTTCAGGAGTCGGGACCTGCTCGTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120  
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 DB 113 CAGCTTCAGGAGTCAGACCTGACCTGGTGAACCTTCTCAGTCACTTCTCACTCACCTGC 172  
 |||||  
 QY 121 ACTGTCACTGGTACTCAATCACAGTGATCATGCCCTGGA-GCTGGATCCGGCAGTTTCC 179  
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 DB 173 ACTGTCACTGGTACTCCATCACAGTGGTATTGGCTGGACACTGGATCCGGCAGTTTCC 232  
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 QY 180 AGGAAACAAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 239  
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 DB 233 AGGAAACAAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 292  
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 QY 240 ATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTCTACA 299  
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FEATURES  
 source

Db 293 ATCTCTCAAAAGTCGAATCTCTCTTACTCGAGACACATCCAAAGAACCAAGTCTTCTCTGCAG 352  
 QY 300 GTTGAAATCTGTGACTACTGTGGGACACGTCACATATTACTGTGCAAGA 348  
 Db 353 GTTGAATCTGTGACTACTGTAGGACACAGCCACATATTACTGTGCAAGA 401

RESULT 12  
 BF580560 866 bp mRNA linear EST 12-DEC-2000  
 LOCUS 602097363F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4217294 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF580560  
 VERSION BF580560.1 GI:11654272  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 866)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM9795 row: n column: 15  
 High quality sequence stop: 681.

FEATURES  
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 1..866  
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 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4217294"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Co24"  
 /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.6 Kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 217 a 231 c 220 g 198 t  
 ORIGIN

Query Match 71.0%; Score 291.8; DB 10; Length 866;  
 Best Local Similarity 91.9%; Pred. No. 2.8e-74;  
 Matches 319; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
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 QY 61 CAGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120  
 Db 101 CAGCTTCAGGAGTCAGGACCTGGCCTGGTGAACCTTCTCAGTCTCTGTCGACCTGC 160  
 QY 121 ACTGTCACTGGTCTCAATACCAAGTATCATGCTGGAGTGGATCGGCGAGTTTCCA 180  
 Db 161 ACTGTCACTGGTCTCAATACCAAGTATCATGCTGGAGTGGATCGGCGAGTTTCCA 220  
 QY 181 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240  
 Db 221 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 280  
 QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTCTTCTCTACAG 300

Db 281 TCTCTCAAAAGTCGAATCTCTGTTTACTCGAGACACATCCAAAGAACCAAGTCTTCTCTGCAG 340  
 QY 301 TTGAATTTCTGTGACTACTGTGGGACACGTCACATATTACTGTGCAAG 347  
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RESULT 13  
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 LOCUS 602095092F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4209454 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF579775  
 VERSION BF579775.1 GI:11653487  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 954)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM9775 row: g column: 23  
 High quality sequence stop: 608.

FEATURES  
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 /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 226 a 275 c 247 g 206 t  
 ORIGIN

Query Match 70.9%; Score 291.2; DB 10; Length 954;  
 Best Local Similarity 84.6%; Pred. No. 4.3e-74;  
 Matches 352; Conservative 0; Mismatches 59; Indels 6; Gaps 2;  
 QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATG 60  
 Db 13 ATGAGAGTCTGATTC-TTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATG 71  
 QY 61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120  
 Db 72 CAACTTCAGGAGTCAGGACCTGACCTGGTGAACCTTCTCAGTCACTTCACTCACCTGC 131  
 QY 121 ACTGTCACTGGTCTCAATCACCAGTATCATGCTGGAGTGGATCGGCGAGTTTCCA 180  
 Db 132 ACTGTCACTGGTCTCAATCACCAGTGGTATGCCTGGCCTGGTCCGCGAGTTTCCA 191  
 QY 181 GGAACAACACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240  
 Db 192 GGAACAACACTGGAGTGGGTCCATACCTACAGTGGTAGTAGTAATTCACACCCA 251  
 QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAAGTCTTCTCTACAG 300  
 Db 252 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAGGAACCAAGTCTTCTCTGCAG 311

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Qy 301 TTGAATCTGTGACTTGGGACACGTCCTCCATATATTACTGTGAAGATCCTAGCTCGG 360
Db 312 TTGAATCTGTGACTTGGGACACGTCCTCCATATATTACTGTGAAGATCCTAGCTCGG 371
Qy 361 ACTAGGCTA-----TGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCCA 411
Db 372 ACAACGAGCTACTTTGACAACTGGGGCCAAAGCACCACCTCTCACAGTCTCCCCA 427

RESULT 14
LOCUS BE309330 741 bp mRNA linear EST 26-OCT-2000
DEFINITION 601093704F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3488305 5',
mRNA sequence.
ACCESSION BE309330
VERSION BE309330.1 GI:9167350
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 741)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8527 row: h column: 02
High quality sequence stop: 572.
Location/Qualifiers
1. 741
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3488305"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 171 a 206 c 174 g 190 t
ORIGIN
Query Match 68.1%; Score 279.8; DB 10; Length 741;
Best Local Similarity 87.9%; Pred. No. 8.2e-71;
Matches 305; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGTGATTTTGTGGCTGTTCACAGCCTTCTCGGTATCCTCTCTGATGTG 60
Db 22 ATGAAGTGTGAGTCTGTGTACCTGTGTGACGCCATCTCGGTATCCTCTCTGATGTA 81
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGTGTGAAGCTTCTCAGTCTGTCTCCCTCACCTGC 120
Db 82 CAGCTTCAGGAGTCAGGACCTGGGCTCGTGAACCTTCTCAGTCTGTCTCTCACCTGC 141
Qy 121 ACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGATCCGCGAGTTTCCA 180
Db 142 TCTGTCACTGCTACTCCATCACCAGTGGTATTACTGGAACTGGATCCGCGAATTTCCA 201
Qy 181 GGAAACAACTGGAGTGGGTGCTACATAAGTTTACAGTGGTATCACTACCTACCAACCA 240

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Db 202 GGAAACAACTGGAAATGGATGGGCTACATAAAATTACGACGGTAGCAATAACTACAACCCA 261
Qy 241 TCTCTCAAAAAGTCGAATCTCTATCAGTCGAGACACATCCCAAGAACCAAGTTCTTCTCTACAG 300
Db 262 TCTCTCAAAAAGTCGAATCTCTATCAGTCGAGACACATCTAAGAACCAAGTTTCTCTGAG 321
Qy 301 TTGAATTTCTGTACTACTGGGACACGTCCTCCATATATTACTGTGTGCAAG 347
Db 322 CTGAATTTCTGTACTACTGAGGACACAGCTACATATTACTGTGTGCAAG 368

RESULT 15
LOCUS BG963270 735 bp mRNA linear EST 12-JUN-2001
DEFINITION 602828371F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983352 5',
mRNA sequence.
ACCESSION BG963270
VERSION BG963270.1 GI:14950907
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 735)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10987 row: m column: 17
High quality sequence stop: 551.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983352"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 172 a 218 c 169 g 176 t
ORIGIN
Query Match 65.9%; Score 271; DB 12; Length 735;
Best Local Similarity 87.2%; Pred. No. 3.1e-68;
Matches 355; Conservative 0; Mismatches 45; Indels 7; Gaps 5;

Qy 1 ATGAGAGTGTGATTTTGTGGCTGTTCACAGCCTTCTCGGTATCCTCTCTGATGTG 60
Db 29 ATGAGAGTGTCTATTCTTTTGTGGCTGTTCACAGCCTTCTCGGTATCCTCTCTGATGTG 88
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCTTCTCAGTCTGTCTCTCACCTGC 120
Db 89 CAGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTGTCTCTCACCTGC 148
Qy 121 ACTGTCACTGGCTACTCAATCACCAG--TGATCATGCTGGAGCTGGATCCGCGAGTTTCC 179
Db 149 ACTGTCACTGGCTACTCCATCACCAGCTGGTTATTACTGGAACCTGGATCCGCGAGTTTCC 208
Qy 180 AGAAACAACTGGAGTGGATGGGCTACA--TAAGTTACAGTGGTATCACTACCTACAACC 238

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Db 209 AGGAAACAACTGGAGTGGGCTACACTATATAATAGTGGTAGCACTAACTACAACC 268  
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Db 269 CATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCGAAGAACCAAGTTCTTCCTGC 328  
Qy 299 AGTTG-AATTCTGTGACTACTGGGGACAC-GTCCACATATTACTGTGCAAGATCCCTAGC 356  
Db 329 AGTTGCACTTCTGTGACGACTGAGGACACAGCCACATATTACTGTGCAAG---TGGAGG 385  
Qy 357 TCGGACTAGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCG 403  
Db 386 GGGTAAGGATACCTTTGACTACTGGGGCCAGGCCACCACCTCTCACGG 432

Search completed: October 24, 2003, 05:48:32  
Job time : 1810.39 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 02:25:30 ; Search time 204.462 Seconds  
(without alignments)  
5426.282 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATGAGAGTGTGATCTTTT.....CCTCAGTCACCGTCTCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 19Jun03.\*

| ID | Score | Match | Length | DB | ID       | Description         |
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| 2  | 322   | 78.3  | 408    | 21 | AAA74604 | Murine 5B3 antibody |
| 3  | 316.8 | 77.1  | 402    | 25 | ABZ23940 | Antibody 806 varia  |
| 4  | 313.4 | 76.3  | 408    | 17 | AAT40804 | Mab 1.4 heavy chai  |
| 5  | 313.4 | 76.3  | 408    | 19 | AAV12261 | Monoclonal antibody |
| 6  | 297.8 | 72.5  | 357    | 18 | AAT56258 | Lead binding Mab 1  |
| 7  | 284.6 | 69.2  | 836    | 16 | AAT04584 | AntiDNP-scfv. Syn   |
| 8  | 284.6 | 69.2  | 836    | 21 | AAZ51113 | Anti-dinitrophenol  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB | ID       | Description         |
|------------|-------|-------|--------|----|----------|---------------------|
| 1          | 411   | 100.0 | 411    | 13 | AAQ30756 | pPM-h1. Synthetic   |
| 2          | 322   | 78.3  | 408    | 21 | AAA74604 | Murine 5B3 antibody |
| 3          | 316.8 | 77.1  | 402    | 25 | ABZ23940 | Antibody 806 varia  |
| 4          | 313.4 | 76.3  | 408    | 17 | AAT40804 | Mab 1.4 heavy chai  |
| 5          | 313.4 | 76.3  | 408    | 19 | AAV12261 | Monoclonal antibody |
| 6          | 297.8 | 72.5  | 357    | 18 | AAT56258 | Lead binding Mab 1  |
| 7          | 284.6 | 69.2  | 836    | 16 | AAT04584 | AntiDNP-scfv. Syn   |
| 8          | 284.6 | 69.2  | 836    | 21 | AAZ51113 | Anti-dinitrophenol  |

|    |       |      |      |    |          |                     |
|----|-------|------|------|----|----------|---------------------|
| 9  | 283   | 68.9 | 836  | 15 | AAQ66698 | Sequence of the si  |
| 10 | 281.2 | 68.4 | 1200 | 20 | AAV90424 | Chimeric antibody   |
| 11 | 280.2 | 68.2 | 357  | 25 | ABZ21158 | Variable region an  |
| 12 | 279.2 | 67.9 | 720  | 14 | AAQ40462 | Fv(FU27). Homo sa   |
| 13 | 277   | 67.4 | 357  | 25 | ABZ21157 | Variable region an  |
| 14 | 274.6 | 66.8 | 378  | 13 | AAQ25667 | Sequence of the an  |
| 15 | 272.8 | 66.4 | 714  | 15 | AAQ67358 | Anti-traseolide 02  |
| 16 | 269   | 65.5 | 354  | 25 | ABZ57952 | Humanised antibody  |
| 17 | 267   | 65.0 | 1002 | 21 | AAA50164 | DNA encoding SH7 s  |
| 18 | 266.2 | 64.8 | 363  | 21 | AAA50159 | Antibody SH7 heavy  |
| 19 | 265.8 | 64.7 | 357  | 25 | ABZ21160 | Variable region an  |
| 20 | 264.4 | 64.3 | 354  | 17 | AAT39555 | Variable heavy cha  |
| 21 | 264.4 | 64.3 | 354  | 18 | AAT69539 | Anti-human FasL an  |
| 22 | 260.8 | 63.5 | 411  | 21 | AAA30416 | Mouse VH group I(A  |
| 23 | 260   | 63.3 | 639  | 16 | AAQ80291 | Monoclonal antibod  |
| 24 | 259.4 | 63.1 | 354  | 25 | ABZ57951 | Humanised antibody  |
| 25 | 258.2 | 62.8 | 366  | 19 | AAV09790 | DNA encoding the h  |
| 26 | 257.8 | 62.7 | 354  | 25 | ABZ57950 | Humanised antibody  |
| 27 | 255.8 | 62.2 | 426  | 18 | AAT73902 | Variable heavy sub  |
| 28 | 255.8 | 62.2 | 426  | 20 | AAZ28410 | Antibody 24-31 hum  |
| 29 | 255.8 | 62.2 | 426  | 24 | ABX03771 | Murine wild-type a  |
| 30 | 253.4 | 61.7 | 366  | 19 | AAV09792 | DNA encoding the h  |
| 31 | 250.4 | 60.9 | 746  | 18 | AAT62573 | scFv(1.1ASML) gene  |
| 32 | 250.2 | 60.9 | 351  | 11 | AAQ06214 | VH domain of antib  |
| 33 | 250.2 | 60.9 | 351  | 17 | AAT63503 | Monoclonal antibody |
| 34 | 250.2 | 60.9 | 351  | 17 | AAT36663 | Monoclonal antibody |
| 35 | 245.6 | 59.8 | 420  | 19 | AAV09801 | DNA encoding the h  |
| 36 | 245.4 | 59.7 | 420  | 19 | AAV09803 | DNA encoding the h  |
| 37 | 244.8 | 59.6 | 847  | 21 | AAQ96550 | Nucleotide sequenc  |
| 38 | 244   | 59.4 | 830  | 13 | AAQ30714 | Sequence of PCR pr  |
| 39 | 243.8 | 59.3 | 1135 | 22 | AAV76338 | Anti-VHSV single c  |
| 40 | 243.4 | 59.2 | 2010 | 20 | AAV99657 | Fusion protein L49  |
| 41 | 242.4 | 59.0 | 798  | 13 | AAQ30706 | Sequence of Clone   |
| 42 | 242.4 | 59.0 | 798  | 15 | AAQ44642 | Rd phage clone seq  |
| 43 | 236.6 | 57.6 | 426  | 18 | AAT73900 | Humanised variable  |
| 44 | 236.6 | 57.6 | 426  | 20 | AAZ28408 | Antibody 24-31 hum  |
| 45 | 236.6 | 57.6 | 426  | 24 | ABX03769 | Murine humanised a  |

#### ALIGNMENTS

##### RESULT 1

AAQ30756

ID AAQ30756 standard; cDNA; 411 BP.

XX AC AAQ30756;

XX DT 25-MAR-2003 (updated)

XX DT 30-MAR-1993 (first entry)

XX DE pPM-h1.

XX KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;

XX KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;

XX KW plasmid; pPM-k3; pPM-h1; ss.

XX OS Synthetic.

XX FH Key

XX sig\_peptide

XX mat\_peptide

XX Location/Qualifiers

XX 1..54

XX /\*tag= a

XX 55..411

XX /\*tag= b

XX WO9219759-A1.

XX PD 12-NOV-1992.

XX PF 24-APR-1992; 92WO-JP00544.

XX PR 25-APR-1991; 91JP-0095476.

XX PR 19-FEB-1992; 92JP-0032084.



AB223940  
 ID AB223940 standard; DNA; 402 BP.  
 XX  
 AC AB223940;  
 XX  
 DT 18-MAR-2003 (first entry)  
 XX  
 DE Antibody 806 variable heavy chain (VH) region encoding DNA.  
 XX  
 KW Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;  
 KW monoclonal antibody; mAb 806; antibody therapy; tumour; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..402  
 FT /\*tag= a  
 FT sig\_peptide 1..54  
 FT /\*tag= b  
 FT mat\_peptide 55..402  
 FT /\*tag= c  
 FT /\*note= "806 VH region"  
 XX  
 WO200292771-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 13-MAY-2002; 2002WO-US15185.  
 XX  
 PR 11-MAY-2001; 2001US-290410P.  
 PR 28-SEP-2001; 2001US-326019P.  
 PR 21-DEC-2001; 2001US-342258P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritter G;  
 PI Jungbluth A, Stockert E, Collins P, Caveness WK, Huang H;  
 PI Burgess AM, Nice EC;  
 DR WPI; 2003-129282/12.  
 DR P-PSDB; ABB82796.  
 XX  
 Novel specific binding members, particularly antibodies recognizing  
 PT epidermal growth factor receptor epitope found only in tumorigenic  
 PT cells, useful for diagnosing, preventing and treating cancer in mammals  
 PT  
 XX  
 PS Claim 40; Fig 14A; 123pp; English.  
 XX  
 CC The invention relates to an isolated specific binding member (I) which  
 CC recognizes an epidermal growth factor receptor (EGFR) epitope which is  
 CC found in tumorigenic, hyperproliferative or abnormal cells and not  
 CC detectable in normal cells. The EGFR epitope is located within the region  
 CC comprising residues 273-501 of EGFR and does not demonstrate any amino  
 CC acid sequence alterations or substitutions from normal EGFR. (I) is  
 CC capable of binding the de2-7 EGFR at an epitope distinct from the  
 CC junctional peptide and does not bind to EGFR on normal cells in the  
 CC absence of aberrant expression, or in the absence of amplification of  
 CC normal wild-type gene. The binding member comprises the VH and VL  
 CC polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for  
 CC treating or diagnosing human or animal body, especially for treating  
 CC tumour in a human. (I) is useful for the preparation of a medicament and  
 CC for preventing or treating cancer which is located in or adjacent the  
 CC brain, in a mammal. (I) is also useful for detecting the presence of  
 CC amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation; where  
 CC EGFR is measured by contacting a biological sample from a mammal in which  
 CC the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose  
 CC glycosylation is suspected with (I) under conditions that allow binding  
 CC of the EGFR to the antibody to occur, and detecting whether binding has  
 CC occurred between the EGFR from the sample and the antibody, where the  
 CC detection of binding indicates that presence or activity of the EGFR in  
 CC the sample. This method is useful for detecting cancer in mammals by  
 CC detecting the presence or activity of an EGFR which indicates the

CC existence of a tumour or cancer in the mammal. A pharmaceutical  
 CC composition comprising (I), and optionally vehicle, carrier or diluent is  
 CC useful for preventing and/or treating cancer in mammals, especially for  
 CC treating brain-resident cancers that produce aberrantly expressed EGFR in  
 CC mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic  
 CC astrocytoma or neoplastic arteriovenous malformations, and malignant  
 CC neural tumours in mammals. The present sequence represents the mAb 806  
 CC VH region encoding DNA.  
 XX  
 SQ Sequence 402 BP; 91 A; 102 C; 97 G; 112 T; 0 other;  
 Query Match 77.1%; Score 316.8; DB 25; Length 402;  
 Best Local Similarity 88.0%; Pred. No. 1.3e-89;  
 Matches 345; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 QY 1 ATGAGAGTGTGATTTCTTTTGGCTGTTTCACAGCCTTTCTCGTATCTCTGTGATGTG 60  
 DB 1 ATGAGAGTGTGATTTCTTTTGGCTGTTTCACAGCCTTTCTCGTATCTCTGTGATGTG 60  
 QY 61 CAGCTTCAGGAGTCGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120  
 DB 61 CAGCTTCAGGAGTCGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120  
 QY 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180  
 DB 121 ACTGTCACTGGCTACTCAATCACCAGTGATTTTGCCTGGAACCTGGATCCGGCAGTTTCCA 180  
 QY 181 GGAACAACACTGGAGTGGATGGCTACATAAGTTACAGTGTATCTACTACTCAACACCCA 240  
 DB 181 GGAACAACACTGGAGTGGATGGCTACATAAGTTATAGTGTAACTAGTAGTAACACCCA 240  
 QY 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTCTCTACAG 300  
 DB 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAATTTCTTCTCGAG 300  
 QY 301 TTGAATTTCTGTGACTCTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
 DB 301 TTGAATTTCTGTGACTATTGAGGACACAGCCACATATTACTGTGTAAACGGCGGCGGG 360  
 QY 361 ACTACGGCTATGGACTACTGGGGTCAAGGAAC 392  
 DB 361 TTCTCTTATTGGGGCCAAAGGACTCTGGTCAC 392  
 RESULT 4  
 AAT40804  
 ID AAT40804 standard; cDNA to mRNA; 408 BP.  
 XX  
 AC AAT40804;  
 XX  
 DT 10-FEB-1997 (first entry)  
 XX  
 DE MAb 1.4 heavy chain, directed against type II phospholipase A2.  
 XX  
 KW Monoclonal antibody; phospholipase; myocardial infarction;  
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;  
 KW chronic rheumatism; adult respiratory distress syndrome;  
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma;  
 KW ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..408  
 FT /\*tag= a  
 FT /product= Monoclonal antibody heavy chain.  
 XX  
 PN WO9620959-A1.  
 XX  
 PD 11-JUL-1996.  
 XX  
 PF 27-DEC-1995; 95WO-JP02714.  
 XX

```
PR 29-DEC-1994; 94JP-0340006.
XX (YAMA ) YAMANOUCHI PHARM CO LTD.
XX Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;
PI WPI; 1996-333946/33.
DR P-PSDB; AAW01144.
XX Monoclonal antibody inhibiting type II phospholipase A2 activity -
PT for treatment of myocardial and cerebral infarction
XX Example 6; Figure 11; 69pp; Japanese.
XX Monoclonal antibodies which inhibit type II phospholipase A2 are
CC useful in the treatment of myocardial infarction, cerebral
CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,
CC pancreatitis, adult respiratory distress syndrome and colitis. The
CC antibodies were generated by immunising Balb/C mice with recombinant
CC human type II phospholipase A2. Spleen cells from the mice were
CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas
CC obtained were screened for phospholipase A2 inhibitory activity.
CC Active clones were isolated including 12H5, 1.4 and 10.1. These
CC were cultured and the antibody isolated from the culture
CC supernatant by precipitation with ammonium sulphate and purification
CC on a column of protein A-Sepharose CL4B. Because the antibody acts
CC on the primate and mouse forms of enzyme as well as human it is
CC particularly suitable for preclinical testing.
XX Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
SQ Query Match 76.3%; Score 313.4; DB 17; Length 408;
Best Local Similarity 86.9%; Pred. No. 1.5e-88;
Matches 357; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCTCTGTCGATGTG 60
DB 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCTCTGTCGATGTG 60
QY 61 CAGCTTCAGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 61 CAGCTTCAGGAATCGGGACCTGGCTGGTGAACCTTCTCAATCTCTGTCCTCACCTGC 120
QY 121 ACTGTCAGTGGTCTACTCAATCACTACCTGATGATGCTGGAGTGGATCGGCAGTTTCCA 180
DB 121 ATGGTCACTGGTCTACTCAATCACTACCTGATGATGCTGGAGTGGATCGGCAGTTTCCG 180
QY 181 GGAACAAACTCGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
DB 181 GGAACAAACTCGAGCGGATGGGATACATAAGTACAGTGGTATCACTAGCTACCAACCCA 240
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGCAGTCTTCTCTACAG 300
DB 241 TCTCTCAAAAGTCGAATCTTTATCAGCGGAGACACATCCCAAGCAGTCTTCTCTACAT 300
QY 301 TTGAACTTCTGACTACTCGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
DB 301 TTGACTTCTGACTACTGAGGACAGCAGCCATATTACTGTACAGAGACTTGG---AC 357
QY 361 ACTACGGCTATGACTACTCTGGGCTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 358 GCCTGTACTTCGATGTTTGGGGCGGAGGACACCGTCACCGTCTCCTCA 408
RESULT 5
AAV12261
ID AAV12261 standard; cDNA to mRNA; 408 BP.
XX
AC AAV12261;
XX
XX 16-JUN-1998 (first entry)
DE Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.
```

```
XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
KW amelioration; kidney disorder; nephrotoxicity; anticancer; ds.
XX Unidentified.
XX Location/Qualifiers
FH 1.408
FT /*tag= a
FT /product= "monoclonal antibody 1.4 heavy chain"
FT /note= "no stop codon given"
XX
PN WO9749427-A1.
XX
PD 31-DEC-1997.
XX
PF 27-JUN-1997; 97WO-JP02241.
XX
PR 19-SEP-1996; 96JP-0247635.
PR 27-JUN-1996; 96JP-0167286.
XX (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
XX Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;
XX WPI; 1998-076914/07.
XX P-PSDB; AAW44169.
XX
PT Amelioration of kidney disorders caused by cisplatin administration
PT - by treatment with an antibody inhibiting type II phospholipase A2
PT activity
XX
PS Disclosure; Page 36-37; 74pp; Japanese.
XX
CC The present sequence encodes the monoclonal antibody 1.4 heavy chain
CC against type II phospholipase A2, from the present invention. The
CC present invention describes a novel method for the amelioration of
CC kidney disorders (such as acute renal failure) associated with the
CC administration of cisplatin for the treatment of cancer. The method
CC comprises treatment with a monoclonal antibody which inhibits the
CC activity of type II phospholipase A2 (particularly of type II
CC phospholipase A2 of human origin), or with a protein or peptide
CC possessing the same inhibitory activity and containing a part of the
CC antibody sequence. Preferably the antibody also inhibits the activity of
CC ape and/or mouse type II phospholipase A2, and has the ability to
CC release type II phospholipase A2 bound to a cell membrane. Three
CC specific monoclonal antibodies having these properties which can be
CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,
CC FERM BP-5298 and FERM BP-5297, respectively. The method can be used for
CC suppressing the nephrotoxicity which is a characteristic feature of
CC cisplatin administration, and therefore allowing more efficient use of
CC this drug as an anticancer agent, e.g. by allowing an increased dosage
CC to be used.
XX Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
SQ Query Match 76.3%; Score 313.4; DB 19; Length 408;
Best Local Similarity 86.9%; Pred. No. 1.5e-88;
Matches 357; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCTCTGTCGATGTG 60
DB 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCTCTGTCGATGTG 60
QY 61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 61 CAGCTTCAGGAATCGGGACCTGGCTGGTGAACCTTCTCAATCTCTGTCCTCACCTGC 120
QY 121 ACTGTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 121 ACTGTCAGTGGTCTACTCAATCACTACCTGATGATGCTGGAGTGGATCGGCAGTTTCCA 180
QY 181 GGAACAAACTCGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 180
DB 181 GGAACAAACTCGAGCGGATGGGATACATAAGTACAGTGGTATCACTAGCTACCAACCCA 180
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGCAGTCTTCTCTACAG 300
DB 241 TCTCTCAAAAGTCGAATCTTTATCAGCGGAGACACATCCCAAGCAGTCTTCTCTACAT 300
QY 301 TTGAACTTCTGACTACTCGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
DB 301 TTGACTTCTGACTACTGAGGACAGCAGCCATATTACTGTACAGAGACTTGG---AC 357
QY 361 ACTACGGCTATGACTACTCTGGGCTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 358 GCCTGTACTTCGATGTTTGGGGCGGAGGACACCGTCACCGTCTCCTCA 408
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Db 181 GGAACAACTGGAGCGGATGGGATACATAAGGTACAGTGGTTACACTAGCTCAACCCCA 240  
Qy 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTCCCTACAG 300  
Db 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTCCCTACAT 300  
Qy 301 TTGAATTTCTGTACTACTGGGACACGTCCACATATTACTGTGTGAAGATCCCTAGTCTGG 360  
Db 301 TTGAATTTCTGTACTACTGGGACACGTCCACATATTACTGTGTGAAGATCCCTAGTCTGG 360  
Qy 361 ACTACGGCTATGGACTACTGGGTCAGGACCTCAGTCAACCTCAGTCAACCTCCTCA 411  
Db 358 GCCTGGTACTTCGATGTTTGGGGCGCAGGACCAACGCTCAGTCAACCTCCTCA 408

RESULT 6  
AAT58258  
ID AAT58258 standard; cDNA; 357 BP.  
XX AC AAT58258;  
XX DT 22-AUG-1997 (first entry)  
XX DE Lead binding MAB 13D10 heavy chain variable region encoding cDNA.  
XX KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
XX KW heavy metal; ss.  
XX OS Mus musculus.  
XX XX  
XX FH Key Location/Qualifiers  
XX FT 1. 357  
XX FT /\*tag= a  
XX FT /note= "no stop codon given"  
XX FT  
XX PN WO9639518-A1.  
XX XX  
XX PD 12-DEC-1996.  
XX XX  
XX PF 05-JUN-1996; 96WO-US09258.  
XX XX  
XX PR 10-OCT-1995; 95US-0541373.  
XX PR 05-JUN-1995; 95US-0462798.  
XX XX  
XX PA (BION-) BIONEERASKA INC.  
XX XX  
XX PI Lopez O, Murray PJ, Wylie DE;  
XX XX  
XX DR WPI; 1997-043140/04.  
XX DR P-PSDB; AAW01584.  
XX XX  
XX PT DNA encoding heavy metal binding polypeptide sequences - used for  
XX PT detecting, removing, adding or neutralising heavy metals, such as  
XX PT lead cations  
XX XX  
XX PS Claim 1; Page 70; 125pp; English.  
XX XX  
XX CC The present sequence encodes the heavy chain variable region for  
XX CC monoclonal antibody (MAB) 13D10, which immunoreacts with a lead cation.  
XX CC The sequence was derived from RNA isolated from hybridoma cells from  
XX CC mouse spleen cells. The protein can be used for binding heavy metals,  
XX CC such as lead cations. It can be used for detecting, removing, adding  
XX CC or neutralising the heavy metals in biological and inanimate systems.  
XX CC It can be used in e.g. aqueous liquid systems, in biological or  
XX CC environmental systems or in such compositions as perfumes, cosmetics,  
XX CC pharmaceuticals, health care products, skin treatment products,  
XX CC pesticides, herbicides, solvents used in the production of semi-  
XX CC conductor and integrated circuit components and production materials  
XX CC for electronic components.  
XX XX  
XX SQ Sequence 357 BP; 91 A; 100 C; 79 G; 87 T; 0 other;

Query Match 72.5%; Score 297.8; DB 18; Length 357;  
Best Local Similarity 89.6%; Pred. No. 1.2e-83;  
Matches 320; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
Qy 55 GATGTGACGTTTCAGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGTCCCTC 114  
Db 1 GATGTGACGTTTCAGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGTCCCTC 60  
Qy 115 ACCTGCACTGTCTACTGGTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCCGGCAG 174  
Db 61 ACCTGCACTGTCTACTGGTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCCGGCAG 120  
Qy 175 TTTCAGGAAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCATTACCTAC 234  
Db 121 TTTCAGGAAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCATTACCTAC 180  
Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCCAAGATCCCTA 294  
Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCCAAGATCCCTA 240  
Qy 295 CTACAGTTGAATTTCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCGGT 354  
Db 241 CTGAGTTGAATTTCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCGGT 300  
Qy 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACCTCTCTCA 411  
Db 301 AACTACCCGGTGTACTTTGACTACTGGGGCAAGGCACCACTCTCACAGTCTCTCA 357

RESULT 7  
AAT04584  
ID AAT04584 standard; DNA; 836 BP.  
XX AC AAT04584;  
XX DT 09-APR-1996 (first entry)  
XX DE AntiDNP-scFv.  
XX XX  
XX KW Antibody; scFv; targeting peptide; retroviral vector; gene therapy;  
XX KW adenosine deaminase deficiency; ADA; cancer; hapten dinitrophenol; ss.  
XX OS Synthetic.  
XX PN WO9523846-A1.  
XX XX  
XX PD 08-SEP-1995.  
XX XX  
XX PF 03-MAR-1995; 95WO-US02537.  
XX XX  
XX PR 04-MAR-1994; 94US-0205980.  
XX XX  
XX PA (UNYNE-) UNIV NEW JERSEY.  
XX XX  
XX PI Dornburg RC;  
XX XX  
XX DR WPI; 1995-320563/41.  
XX XX  
XX PT Retroviral vectors for use in cell specific gene transfer - contain  
XX PT antibody-envelope and wild-type envelope-fusion proteins  
XX XX  
XX PS Example; Fig 3; 35pp; English.  
XX XX  
XX CC The anti-hapten dinitrophenol single chain antibody (anti-DNP scFv)  
XX CC encoded by this sequence is used as a targeting peptide (TP), which is  
XX CC fused to the envelope protein of a retroviral vector. When the TP is  
XX CC fused to the envelope protein, it replaces or disrupts the natural  
XX CC receptor binding site. By using a TP that recognises a cell surface  
XX CC antigen, the retroviral vectors containing TP's can be used in a cell  
XX CC type specific method for introducing genes into cells. These retroviral  
XX CC vectors can be used in the gene therapy of human genetic diseases  
XX CC including, adenosine deaminase (ADA) deficiency, and in clinical trials





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Db 254 TCTCTCAAAATCGAATCTCCATCTCTGTCGACATCTAAGAACCCAGTTTTCTCTGAAG 313
Qy 301 TTGAATTCGTCTACTCTGGGACACAGCTCCACATATTACTGTGCAAGATCCCTAG---CT 357
Db 314 TTGAATTCGTCTACTCTGGGACACAGCTCCATATTACTGTGCAAGAGATAGAGGGTAT 373
Qy 358 CGGACTACGGCTATGAGCTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 374 GACCACGGGGGTTTGCTTACTGGGGCAAGGACTCTGCTCAGTCTCTCTGCA 427

RESULT 11
ID ABZ21158 standard; DNA; 357 BP.
XX ABZ21158;
XX
XX 28-MAR-2003 (first entry)
XX
XX Variable region anti-bisphenol A antibody chain coding sequence #2.
XX
XX Variable region; anti-bisphenol A; antibody; murine; heavy chain;
XX light chain; gene; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..357
XX FT /*tag= a
XX FT /partial
XX FT /product= "Variable region anti-bisphenol A antibody
XX *FT chain #2"
XX FT /note= "No start or stop codon given"
XX
XX JP2002253259-A.
XX
XX 10-SEP-2002.
XX
XX 02-MAR-2001; 2001JP-0058673.
XX
XX 02-MAR-2001; 2001JP-0058673.
XX
XX (BIOS-) BIO APPLIED SYSTEMS KK.
XX
XX WPI: 2003-096537/09.
XX P-PSDB; ABB98906.
XX
XX Gene encoding anti-bisphenol A antibody, a recombinant protein and its
XX preparation, a DNA, a vector, a transformant, preparation of a
XX recombinant protein, a kit for determining bisphenol A -
XX
XX Claim 1; Page 11; 19pp; Japanese.
XX
XX The present invention relates to sequences for murine heavy chain
XX variable region or light chain variable region of anti-bisphenol A
XX antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are
XX useful for the preparation of recombinant protein.
XX
XX Sequence 357 BP; 94 A; 92 C; 79 G; 92 T; 0 other;
XX
XX Query Match 68.2%; Score 280.2; DB 25; Length 357;
XX Best Local Similarity 86.6%; Pred. No. 4.1e-78;
XX Matches 309; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
XX
Qy 55 GATGTGCAAGTTTCAGGAGTCGGGACCTGTCTGTGTTGAAGCCCTTCTCAGTCTCTGTCCTC 114
Db 1 GATGTACAGTTTCAGGAGTCAGGACCTGTGCTCGTGAACCTTCTCAGTCTCTGTCCTC 60
Qy 115 ACCTGCAGTCTCAGTGGTACTCAATCACCAGTATCATGCTGAGCTGGATCCGGCAG 174
Db 61 ACCTGCTCTGCTCAGTGGTACTCCATCCAGTGGTTATTACTGGAAGTGGATCCGGCAG 120
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGGTACTACTACCTAC 234

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Db 121 TTTTCAGGAAACAAATGGAATGATGGCTTACATAAGGTACGAGGTAGCAATAACTAC 180
Qy 235 AACCATCTCTCAAAAGTCGAATCTCTATCTACTCGAGACACATCCAAGAACCAAGTTCTTC 294
Db 181 AACCATCTCTCAAAATCGAATCTCCATCTACTCGTACACATCTAAGAACCAAGTTTTC 240
Qy 295 CTACAGTTGAATTCGTGACTACTGGGACACAGTCCACATATTACTGTGCAAGATCCCTCA 354
Db 241 CTGAAGTTGAATTCGTGACTACTGAGACACAGTACATATTACTGTGCAAGATATTG 300
Qy 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 301 GGACGGGGCTATGTTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 357

RESULT 12
AAQ40462
ID AAQ40462 standard; DNA; 720 BP.
XX
XX AC AAQ40462;
XX
XX 25-MAR-2003 (updated)
XX 20-AUG-1993 (first entry)
XX
XX Fv(TU27).
XX
XX pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
XX heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
XX immunomodulator; immunosuppressant; graft rejection; allergy;
XX autoimmune disease; leukemia; cyclosporin; ss.
XX
XX Homo sapiens.
XX
XX EP539748-A1.
XX
XX 05-MAY-1993.
XX
XX 30-SEP-1992; 92EP-0116746.
XX
XX 03-OCT-1991; 91JP-0256335.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX Hamuro J, Shimamura T, Taki S;
XX
XX WPI; 1993-145163/18.
XX P-PSDB; AAR34510.
XX
XX Polypeptide(s) which bind H chain of human IL-2 receptors - for
XX treating inflammatory, allergic and auto-immune disorders,
XX leukaemias etc.
XX
XX Claim 6; Page 20; 27pp; English.
XX
XX The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
XX polypeptides consisting only of the V regions were purified and
XX sequenced. The polypeptides are capable of binding to the beta
XX chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
XX receptor. They are useful as immunomodulators and
XX immunosuppressants, e.g. to prevent graft rejection or to treat
XX inflammatory allergic and autoimmune diseases, or leukemia. Unlike
XX cyclosporin etc. they are both effective and safe.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 720 BP; 186 A; 188 C; 170 G; 176 T; 0 other;
XX
XX Query Match 67.9%; Score 279.2; DB 14; Length 720;
XX Best Local Similarity 88.5%; Pred. No. 1.1e-77;
XX Matches 315; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
XX
Qy 56 ATGTGCAAGTTTCAGGAGTCGGGACCTGTCTGTGTTGAAGCCCTTCTCAGTCTCTGTCCTCA 115

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Db 368 AGGTCAAACTCGAGGAGTCTGGACCTGGCCCTGGTGAACCTTCTCAGTCTCTGTCCCTCA 427  
 QY 116 CCTGCACTGTCACTGGCTACTCAATCACCAGTGTATGCTCGGAGCTGGATCGGCAGT 175  
 Db 428 CCTGCACTGTCACTGGCTACTCAATCACCAGTGTATGCTCGGAGCTGGATCGGCAGT 487  
 QY 176 TTCCAGGAACAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACCTACA 235  
 Db 488 TTCCAGGAACAACAACTGGAGTGGGCTACGTAAGCTACAGTGGTAGCACTGACTACA 547  
 QY 236 ACCCATCTCTCAAAAGTCGAATCTCTATCATCTCGAGACACATCCAAAGAACAGTTCTTC 295  
 Db 548 ACCCATCTCTCAAAAGTCGAATCTCTATCATCTCGAGACACATCCAAAGAACAGTTCTTC 607  
 QY 296 TACAGTTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAG 355  
 Db 608 TGCAGTTGAATCTGTGACTACTGAGACACAGCCACATATTACTGTGCAAGA---GGTG 664  
 QY 356 CTCGGACTACGGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
 Db 665 GTTTCCTCTATGCTATGGACTACTGGGCTCAAGGACACCGTCACCGTCTCTCTCA 720

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 XX ABZ21157;  
 AC  
 XX 28-MAR-2003 (first entry)  
 DT  
 DE Variable region anti-bisphenol A antibody chain coding sequence #1.  
 XX  
 KW Variable region; anti-bisphenol A; antibody; murine; heavy chain;  
 KW light chain; gene; ds.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..357  
 FT /\*tag= a  
 FT /partial  
 FT /product= "Variable region anti-bisphenol A antibody  
 chain #1"  
 FT /note= "No start or stop codon given"  
 FT  
 PN JP2002253259-A.  
 XX  
 XX 10-SEP-2002.  
 XX  
 XX 02-MAR-2001; 2001JP-0058673.  
 XX  
 PR 02-MAR-2001; 2001JP-0058673.  
 XX  
 XX (BIOS-) BIO APPLIED SYSTEMS KK.  
 XX  
 XX WPI; 2003-096537/09.  
 DR P-FSDB; ABB98905.  
 XX  
 XX Gene encoding anti-bisphenol A antibody, a recombinant protein and its  
 PT preparation, a DNA, a vector, a transformant, preparation of a  
 PT recombinant protein, a kit for determining bisphenol A -  
 XX  
 XX Claim 1; Page 10; 19pp; Japanese.  
 PS  
 CC The present invention relates to coding sequences for murine heavy chain  
 CC variable region or light chain variable region of anti-bisphenol A  
 CC antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are  
 CC useful for the preparation of recombinant protein.  
 XX  
 SQ Sequence 357 BP; 94 A; 91 C; 79 G; 93 T; 0 other;  
 Query Match 67.4%; Score 277; DB 25; Length 357;

Best Local Similarity 86.0%; Pred. No. 4.2e-77;  
 Matches 307; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
 QY 55 GATGTGAGCTTCAGGAGTCGGACCTGTCTCGTGAAGCTTCTCAGTCTCTGTCCCTC 114  
 Db 1 GATGTGAGCTTCAGGAGTCGGACCTGTCTCGTGAAGCTTCTCAGTCTCTGTCTCTC 60  
 QY 115 ACCTGCACCTGTCACTGGCTACTCAATCACCAGTGTATGCTCGGAGCTGGATCCGCGAG 174  
 Db 61 ACCTGCTCTGCTACTGGCTACTCCATCACCAGTGGTTATTACTTGAAGTGGATCCGCGAG 120  
 QY 175 TTTCAGGAACAACAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACTAC 234  
 Db 121 TTTCAGGAACAACAACTGGAGTGGATGGCTATATAAGTGTACGACGGTAGCAATAACTAC 180  
 QY 235 AACCCATCTCTCAAAAGTCGAATCTCTATCATCTCGAGACACATCCAAAGAACAGTTCTTC 294  
 Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCATCTCGGACACATCTAAGAACAGGATTTTC 240  
 QY 295 CTACAGTTGAATCTGTGACTACTGGGACACAGCTCCACATATTACTGTGCAAGATCCCTA 354  
 Db 241 CTGAATTTGAATCTGTGACTCTCTGAGGACACAGCTACATATTACTGTGCAAGATTTG 300  
 QY 355 GCTCGGACTACGGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
 Db 301 GGACGGGCTATGTTGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 357

RESULT 14  
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 ID AAQ25667 standard; cDNA; 378 BP.  
 XX  
 AC AAQ25667;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 28-DEC-1992 (first entry)  
 XX  
 DE Sequence of the anti-urokinase antibody kappa variable region (VK)  
 DE cDNA.  
 XX  
 KW Chimeric monoclonal antibody; anti-urokinase antibody; PCR;  
 KW antithrombotic agent; myocardial infarction therapy; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
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 FT /\*tag= a  
 FT mat\_peptide 10..378  
 FT /\*tag= b  
 FT misc\_feature 1..27  
 FT /\*tag= c  
 FT misc\_feature 18..32  
 FT /label= VH01 primer  
 FT /\*tag= d  
 FT misc\_feature 340..371  
 FT /label= 5'VH1 primer  
 FT /\*tag= e  
 FT misc\_feature 356..371  
 FT /label= 3'mVH primer  
 FT /\*tag= f  
 FT /label= JH01 primer  
 XX  
 PN EP491351-A2.  
 XX  
 XX 24-JUN-1992.  
 XX  
 XX 17-DEC-1991; 91EP-0121591.  
 XX  
 PR 18-DEC-1990; 90JP-0413829.  
 PR 11-NOV-1991; 91JP-0294464.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.

XX Iwasa S, Taka H, Watanabe T, Tada H;  
XX WPI; 1992-209528/26.  
DR P-PSDB; AAR24722.  
XX Chimeric monoclonal antibodies - contain anti-human fibrin  
PT antibody light and heavy chain variable and constant for treating  
PT thrombotic conditions e.g. myocardial infarction  
XX  
PS Example; Figure 15; 87pp; English.  
XX  
XX Poly(A) + RNA was prep'd. from mouse anti-urokinase  
CC antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as  
CC a template, an anti-urokinase antibody VK cDNA was amplified with  
CC the mc-kappa primer as primer for first strand synthesis, and the  
CC 3'/mv-kappa and 5'/mv-kappa primers as primers for the PCR. The  
CC amplified fragment was restriction digested and ligated into a  
CC restriction fragment of pTB1423 to give an anti-urokinase antibody  
CC VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is  
CC given in AAQ25667. The cDNA is a functional VK gene. The sequence of  
CC the primer (mc-gamma-1) is given in AAQ25689.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 378 BP; 92 A; 100 C; 91 G; 95 T; 0 other;  
  
Query Match 66.8%; Score 274.6; DB 13; Length 378;  
Best Local Similarity 86.4%; Pred. No. 2.5e-76;  
Matches 317; Conservative 0; Mismatches 44; Indels 6; Gaps 1;  
  
QY 47 TCTGTCTCATGTGCGACGTTTCAGGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTC 106  
DB 2 TCGACTGTGAGTGCACACTAGTGGAGTCGGGACCTGGCTGTGAACCTTCTCAGTCTC 61  
  
QY 107 TGTCCCTACCTGCACCTGTCAGTCTGCTATCTCAATCACCAGTGCATGCTCGAGCTGGA 166  
DB 62 TGTCCCTACCTGCACCTGTCAGTCTGCTATCTCAATCACCAGTGCATGCTCGAGCTGGA 121  
  
QY 167 TCGGCGAGTTTCAGGAACAACACTGGAGTGGGTGCTACATAAGTACAGTGTATCA 226  
DB 122 TCGGCGAGTTTCAGGAACAACACTGGAGTGGGTGCTACATAAGTACAGTGTATCA 181  
  
QY 227 CTACCTTACACACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACC 286  
DB 182 CTAGTTACACACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCATACCC 241  
  
QY 287 AGTTCTTCTACAGTTGAATCTGTGACTACTGGGACACGTCCTCATATTACTGTGCAA 346  
DB 242 AGTTCTTCTGAGTTGAATCTGTGACTTCTGAGGACACTGCCACATATTACTGTGCAA 301  
  
QY 347 GATCCCTAGCTGGACTACGGCT-----ATGGACTACTGGGGTCAAGGAACCTCAGTCA 400  
DB 302 GATGGGTGATTTCGACGCGGGTGACTACTTTGACTACTTGGGGCCAAGGACCAAGTCA 361  
  
QY 401 CCGTCTC 407  
DB 362 CCGTCTC 368

RESULT 15  
ID AAQ67358  
XX AAQ67358 standard; DNA; 714 BP.  
XX  
AC AAQ67358;  
XX  
DT 25-MAR-2003 (updated)  
DT 27-MAR-1995 (first entry)  
XX  
DE Anti-traseolide 02/01/01 scFv.  
XX  
KW Binding protein; immobilization; chimeric protein;  
KW anchoring protein; Saccharomyces cerevisiae; PUR4143;  
KW musk fragrance; traseolide; polymerase chain reaction;

KW PCR; amplification; primer; light chain; hybridoma; scFv;  
KW single chain antibody; monoclonal antibody; ds.  
XX Synthetic.  
XX WO9418330-A1.  
XX  
XX 18-AUG-1994.  
XX  
XX 10-FEB-1994; 94WO-BP00427.  
XX  
XX 10-FEB-1993; 93EP-0200350.  
XX (UNIL ) UNILEVER NV.  
XX (UNIL ) UNILEVER PLC.  
XX  
XX De Geus P, Frenken LGJ, Klis FM, Toschka HY, Verrips CT;  
XX WPI; 1994-279751/34.  
XX  
XX Immobilised binding proteins for specific cpds - obt'd. by  
PT expressing chimeric proteins comprising the binding protein and a  
PT cell wall-anchoring protein in host cells  
XX  
PS Disclosure; Page 35; 78pp; English.  
XX  
XX Valuable compounds are isolated from complex mixtures by use of  
CC immobilized ligands composed of an anchoring protein and a binding  
CC protein. A gene encoding such a chimeric protein that will anchor  
CC in the cell wall of a lower eukaryote, e.g. S. cerevisiae, and which  
CC binds traseolide with high specificity, was constructed using plasmid  
CC PUR4143. This plasmid contains a gene encoding an scFv-TRAS  
CC fragment of anti-traseolide antibody 02/01/01 (AAQ67358) obtained by  
CC PCR amplification of hybridoma cDNA using primers AAQ67353-34 for  
CC the heavy chain, and primers AAQ67355-56 for the light chain.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 714 BP; 174 A; 188 C; 178 G; 174 T; 0 other;

Query Match 66.4%; Score 272.8; DB 15; Length 714;  
Best Local Similarity 87.9%; Pred. No. 1.2e-75;  
Matches 311; Conservative 0; Mismatches 37; Indels 6; Gaps 1;  
  
QY 64 CTTGAGGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGCTCCCTCACCTGCAC 123  
DB 1 CTGAGGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGCTCCCTCACCTGCAC 60  
  
QY 124 GTCACCTGCTACTCAATCACCAGTCATCATCCCTGGAGCTGGATCCGGCAGTTCCTCCAGGA 183  
DB 61 GTCACCTGCTACTCAATCACCAGTCATCATCCCTGGAGCTGGATCCGGCAGTTCCTCCAGGA 120  
  
QY 184 AACAACTGGAGTGGGTGCTACATAAGTTACAGTGGTATCATTACCTACACCCATCT 243  
DB 121 AACCACTGGAGTGGGTGCTACATAAGTTACAGTGGTATCATTACCTACACCCATCT 180  
  
QY 244 CTCAAAAGTCCAAATCTCTATCACTCGAGACATCCAGAACCTGCTTCCTCAGTTG 303  
DB 181 CTCAAAAGTCCAAATCTCTCTCACTCGAGACATCCAGAACCTGCTTCCTCAGTTG 240  
  
QY 304 AATTCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGGACT 363  
DB 241 AATTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGCTCCCTAACATGGTTA 300  
  
QY 364 ACGGCTATGGA-----CTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411  
DB 301 CTAGCTCGGAACCGTTCTTACTTGGGGCCAAGGGACCAAGGTCACCGTCTCCTCA 354

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Job time : 205.462 secs

GenCore version 5.1.6  
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Perfect score: 411  
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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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7: gb\_ph.\*  
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9: gb\_pr.\*  
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13: gb\_un.\*  
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35: em\_htg\_rnd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
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41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 411   | 100.0         | 411    | 6     | AR024276 Sequence  |
| 2          | 411   | 100.0         | 411    | 6     | AR045129 Sequence  |
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| 4          | 411   | 100.0         | 411    | 6     | E05354 DNA encodin |
| 5          | 411   | 100.0         | 411    | 6     | E05420 cDNA sequen |
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| 9          | 332.2 | 80.8          | 423    | 6     | AX236250 Sequence  |
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| 11         | 329.4 | 80.1          | 399    | 10    | MUSIGHDOB          |
| 12         | 327.8 | 79.8          | 417    | 10    | MMU05284           |
| 13         | 322   | 78.3          | 408    | 6     | AX027688 Sequence  |
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| 18         | 307   | 74.7          | 485    | 10    | MUSIGHAAC          |
| 19         | 302.6 | 73.6          | 358    | 10    | MUSOHP138G         |
| 20         | 298.4 | 72.6          | 492    | 10    | MUSIGHGK           |
| 21         | 297.8 | 72.5          | 357    | 6     | AR108677           |
| 22         | 297.8 | 72.5          | 358    | 10    | MUSOHP7D7G         |
| 23         | 297.4 | 72.4          | 503    | 10    | MUSIGHAAO          |
| 24         | 294.6 | 71.7          | 357    | 10    | MUSIGHAM           |
| 25         | 293.4 | 71.4          | 402    | 10    | MUSIGHNOH          |
| 26         | 292.6 | 71.2          | 470    | 10    | MUSIGHXY           |
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| 29         | 288.2 | 70.1          | 358    | 10    | MUSOHP57G          |
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| 33         | 284.6 | 69.2          | 836    | 6     | AR141689           |
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| 36         | 280.4 | 68.2          | 358    | 10    | MUSOHP1E9G         |
| 37         | 280.2 | 68.2          | 357    | 6     | BD174581 Gene enco |
| 38         | 279.8 | 68.1          | 1549   | 10    | BC002091 Mus muscu |
| 39         | 279.2 | 67.9          | 720    | 6     | E05894 DNA sequenc |
| 40         | 278.2 | 67.7          | 417    | 10    | MMU16690           |
| 41         | 278   | 67.6          | 446    | 10    | MMU252270          |
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| 43         | 277   | 67.4          | 357    | 6     | BD174580 Gene enco |
| 44         | 276.8 | 67.3          | 348    | 10    | MMU16457           |
| 45         | 276.4 | 67.3          | 294    | 10    | AF165121 Mus muscu |

ALIGNMENTS

RESULT 1  
AR024276  
LOCUS  
DEFINITION Sequence 30 from patent US 5795965.  
ACCESSION AR024276  
VERSION AR024276.1 GI:3977570  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 411)  
AUTHORS Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.William.  
TITLE Reshaped human to human interleukin-6 receptor  
JOURNAL Patent: US 5795965-A 30 18-AUG-1998;

AR024276 411 bp DNA linear PAT 05-DEC-1998  
Sequence 30 from patent US 5795965.

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FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
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Db 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTGGTATCTGTCGTGATGTG 60
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QY 121 ACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
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Db 301 TTGAATTCGTGACTACTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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RESULT 2
AR045129
LOCUS 411 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5817790.
ACCESSION AR045129
VERSION AR045129.1 GI:5966594
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 411)
AUTHORS Teuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.William.
TITLE Reshaped human antibody to human interleukin-6 receptor
JOURNAL Patent: US 5817790-A 30 06-OCT-1998;
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTGGTATCTGTCGTGATGTG 60
Db 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTGGTATCTGTCGTGATGTG 60
QY 61 CAGCTTCAGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
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QY 121 ACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
Db 121 ACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
QY 181 GGAACAAACTGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
Db 181 GGAACAAACTGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
QY 241 TCTCTCAAAGTCGATCTCTATCACTCGAGACATCCCAAGAACGAGTTCTTCTCTACAG 300
Db 241 TCTCTCAAAGTCGATCTCTATCACTCGAGACATCCCAAGAACGAGTTCTTCTCTACAG 300
QY 301 TTGAATTCGTGACTACTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 301 TTGAATTCGTGACTACTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
QY 361 ACTACGGCTATGAGTACTTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
Db 361 ACTACGGCTATGAGTACTTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
RESULT 3
BD011353
LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Chimeric antibody against human interleukin-6 receptor.
ACCESSION BD011353
VERSION BD011353.1 GI:18639726
KEYWORDS JP 2001083151-A/27.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 411)
AUTHORS Teuchiya,M., Sato,K., Bendig,M.M., Jones,S.T. and Saldanha,H.W.
TITLE Chimeric antibody against human interleukin-6 receptor
JOURNAL Patent: JP 2001083151-A 27 30-MAR-2001;
COMMENT CHUGAI PHARMACEUTICAL CO LTD
OS Mus sp. (mouse)
PN JP 2001083151-A/27
PD 30-MAR-2001
PF 28-JUL-2000 JP 2000229748
PR PI MASAYUKI TSUCHIYA, KO SATO, MARY MARGARET BENDIGU, PI STEVEN TAREN JONES, PI HOSE WILLIAM SALDANHA
PC G01N33/53,A61K38/00,A61K39/395,A61K39/395,A61P35/00, PC GO1N33/577//C07K16/28, PC C07K19/00,C12N15/09, (C12N15/09,C12R1:91),A61K37/02,C12N15/00, PC (C12N15/00,C12R1:91) CC CC
Key Location/Qualifiers
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FT mat_peptide (55)..(411).
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Location/Qualifiers
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BASE COUNT 95 a 114 c 92 g 110 t
ORIGIN
Query Match 100.0%; Score 411; DB 6; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTGGTATCTGTCGTGATGTG 60
Db 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTGGTATCTGTCGTGATGTG 60
QY 61 CAGCTTCAGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
Db 61 CAGCTTCAGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
QY 121 ACTGTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
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121 ACTGTCTACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGCAGTTTCCA 180
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301 TTGAATTTCTGTACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
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RESULT 4
E05354
LOCUS E05354 411 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding V region of H chain of mouse monoclonal antibody against human interleukin-6 receptor.
ACCESSION E05354
VERSION E05354.1 GI:2173543
KEYWORDS JP 1993227970-A/4.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
AUTHORS Tsuchiya,M., Sato,I., Mearii,M.B., Suteilibun,T.J. and Hose,U.S.
TITLE RECONSTRUCTED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
JOURNAL Patent: JP 1993227970-A 4 07-SEP-1993;
CHUGAI PHARMACEUT CO LTD
COMMENT OS Mus sp. (mouse)
PN JP 1993227970-A/4
PD 07-SEP-1993
PF 19-FEB-1992 JP 1992032084
PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU, SUTEILIBUN TAREN JIYONZU, HOSE UIRIAMU SARUDANA PC
C12N15/13, C07K15/06, C12N15/10, C12P21/08, C12Q1/68//C07K15/28, PC C12N5/20,
PC C12N15/06, C12P21/08, C12R1:91;
CC strandedness: Double;
CC topology: linear;
CC *source: clone=pWM-hl;
FH Key Location/Qualifiers
FT sig_peptide 1..54
FT mat_peptide 55..411.
FT Location/Qualifiers
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BASE COUNT 95 a 114 c 92 g 110 t
ORIGIN
Query Match 100.0%; Score 411; DB 6; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAGTGTGATTTCTTTTGGCTGTTCACAGCCCTTCTCGTATCTCTGTGATGTG 60
Db 1 ATGAGAGTGTGATTTCTTTTGGCTGTTCACAGCCCTTCTCGTATCTCTGTGATGTG 60
Qy 61 CAGCTTCAGGAGTCGGGACCTGCTGCTGGTGAAGCCCTTCTAGTCTCTGCTCCTCAGCTGC 120
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Qy 121 ACTGTCTACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGCAGTTTCCA 180
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Qy 181 GGAACAAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACTCAACACCCA 240
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Qy 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTCTTCTCTACAG 300
Db 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTCTTCTCTACAG 300
Qy 301 TTGAATTTCTGTACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 301 TTGAATTTCTGTACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411

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RESULT 5
E05420
LOCUS E05420 411 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA sequence encoding mouse monoclonal antibody H chain against human IL-6 receptor.
ACCESSION E05420
VERSION E05420.1 GI:2173609
KEYWORDS JP 1993236966-A/27.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
AUTHORS Tsuchiya,M., Sato,I., Mearii,M.B. and Suteilibun,T.J.
TITLE DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
JOURNAL Patent: JP 1993236966-A 27 17-SEP-1993;
CHUGAI PHARMACEUT CO LTD
COMMENT OS (mouse)
PN JP 1993236966-A/27
PD 17-SEP-1993
PF 25-APR-1991 JP 1991095476
PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU, SUTEILIBUN TAREN JIYONZU
PC C12N15/13//C12P21/08;
CC strandedness: Double;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: deposit=MCIMB40362;
CC *source: cell_line=PM1;
CC *source: clone=pWM-hl;
FH Key Location/Qualifiers
FT sig_peptide 1..54
FT mat_peptide 55..411
FT /product="mouse monoclonal antibody H chain against human IL-6 receptor mature peptide".
FT Location/Qualifiers
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/db_xref="taxon:10090"

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BASE COUNT 95 a 114 c 92 g 110 t
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Query Match 100.0%; Score 411; DB 6; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GGAACAAACTGGAGTGGATGGCTACATAAGTTACAGTGGTATCAGTACCTACACGCCA 240
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QY 241 TCTCTCAAAAGTCGAATCTCTATCTGAGACACATCCAGAACACAGTTCTTCTCTACAG 300
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QY 301 TTGAATTTCTGTGACTTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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QY 361 ACTACGGCTATGGACTTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
Db 361 ACTACGGCTATGGACTTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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RESULT 6
LOCUS E43823 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Chimeric antibody against human interleukin-6 receptor.
ACCESSION E43823
VERSION E43823.1 GI:18627756
KEYWORDS JP 2000116391-A/27.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
Chimeric antibody against human interleukin-6 receptor
Patent: JP 2000116391-A 27 25-APR-2000;
CHUGAI PHARMACEUT CO LTD
OS Mus sp. (mouse)
PN JP 2000116391-A/27
PD 25-APR-2000
PF 29-NOV-1999 JP 1999338286
PR
PI MASAYUKI TSUCHIYA, ISAO SATO, BENDIGU MARY MARGARET, PI JONES
STEVEN TAREN,
PI SARUDANA HOSE WILLIAM
PC C12N15/09, C07K16/19, C07K16/26, C07K19/00, C12N5/10, C12P21/08, PC
C12N15/00,
CC C12N5/00
FH Key Location/Qualifiers
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FT mat_peptide (55)..(411)
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BASE COUNT 95 a 114 c 92 g 110 t
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGTCTGATTTCTTTTGTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG 60
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Db 1 ATGAGAGTCTGATTTCTTTTGTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG 60
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Db 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
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QY 301 TTGAATTTCTGTGACTTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 301 TTGAATTTCTGTGACTTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
QY 361 ACTACGGCTATGGACTTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
Db 361 ACTACGGCTATGGACTTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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RESULT 7
LOCUS MMIGVHR2 450 bp mRNA linear ROD 07-MAY-1992
DEFINITION Mouse mRNA for immunoglobulin heavy chain variable region.
ACCESSION X05878 Y00330
VERSION X05878.1 GI:52526
KEYWORDS constant region; Ig heavy chain; variable region.
SOURCE Mus musculus (house mouse)
ORGANISM Mus-musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 450)
Grant,F.J., Levin,S.D., Gilbert,T. and Kindsvogel,W.
Improved RNA sequencing method to determine immunoglobulin mRNA
sequence
Nucleic Acids Res. 15 (13), 5496 (1987)
87260030
MEDLINE 3601683
PUBMED
2 (bases 1 to 450)
Grant,F.J.
Direct Submission
Submitted (31-AUG-1987) Dr. Francis Grant, Zymogenetics, Inc., 2121
North 35th Street, Seattle, Wa 98103, USA
JOURNAL
Location/Qualifiers
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/mol_type="mRNA"
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Best Local Similarity 88.8%; Pred. No. 4.9e-103;  
Matches 365; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
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RESULT 8  
MUSIGHDQA 408 bp mRNA linear ROD 04-JUN-1996  
LOCUS Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.  
DEFINITION L20961

VERSION L20961.1 GI:309344  
KEYWORDS V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 408)  
TITLE Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.  
STRUCTURAL profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)  
MEDLINE 95045941  
PUBMED 7957578  
REFERENCE 2 (bases 1 to 408)  
AUTHORS Iwasaki, Y., Takabatake, H., Monestier, M. and Ferrone, S.  
TITLE Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb

JOURNAL Immunogenetics 42 (2), 90-100 (1995)  
MEDLINE 95331832  
PUBMED 7607710  
FEATURES Location/Qualifiers  
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BASE COUNT 99 a 109 c 92 g 108 t  
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Query Match 81.6%; Score 335.4; DB 10; Length 408;  
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Matches 377; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

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Db 181 GGAACAACTGGAGTGGATGGGTACATAACCTTACAGTGGTATCTAGTACCAATCCA 240

Qy 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACATCCCAAGAACCACTTCTTCTCTACAG 300  
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Qy 301 TTGAATCTGTGACTACTGGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360  
Db 301 TTGAATCTGTGACTACTGGGGACAGTCCACATATTACTGTGCAAGAT-TATCGTGGG 359

Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411  
Db 360 ATTACGAC--TTGACTACTGGGGCCCAAGGCCACCACTCTCAGTCTCTCTCA 408

RESULT 9  
AX236250

LOCUS AX236250 423 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 108 from Patent WO0164749.  
ACCESSION AX236250  
VERSION AX236250.1 GI:15795925

KEYWORDS Mus sp.  
SOURCE Mus sp.

ORGANISM Mus sp.  
REFERENCE 1  
AUTHORS Klotzer, W.S. and Hanna, N.  
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL Patent: WO 0164749-A 108 07-SEP-2001;  
Idex Pharmaceuticals Corporation (US)

FEATURES Location/Qualifiers  
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94 a 116 c 99 g 114 t  
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ORIGIN

|                       |                 |                     |           |             |
|-----------------------|-----------------|---------------------|-----------|-------------|
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| Best Local Similarity | 90.6%;          | Pred. No. 2.9e-101; |           |             |
| Matches 378;          | Conservative 0; | Mismatches 33;      | Indels 6; | Gaps 2;     |

  

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| Db | 121 | ACTGTCACTGGCTCCTCAATCACCAGTGATTATGCCCTGGCAGTGGATCCGGCAGTTTCCA    | 180 |
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| Db | 181 | GGAAACAAACTGGAGTGGATGGGCTACATAAGCTTTCAGTGGTAGCACTGGCTACAACCCA    | 240 |
| Qy | 241 | TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCGAAGAACCAAGTTCTTCTCTACAG  | 300 |
| Db | 241 | TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCGAAGAACCAAGTTCTTCTCTCAG   | 300 |
| Qy | 301 | TTGAATTTCTGTGACTACTGGGGACACGTCACACATATTTACTGTGCAAGA----TCCCTTAGC | 356 |
| Db | 301 | TTGAATTTCTGTGACTACTGAGGACACAGCCACATATTTACTGTGCAAGAGGCTTATGGT     | 360 |
| Qy | 357 | TCGGACTACGGCTA--TGGACTACTGGGTCAAGGAACCTTCAGTCAACGCTCTCTCTCA      | 411 |
| Db | 361 | TATGACGTGGCTACTTTTGACTACTGGGGCAAGGCCACCACTCTCAACGCTCTCTCTCA      | 417 |

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|------------|---|--------|--------|-----------------|
| RESULT 10  | MUSIGHDQC   | 402 bp | linear | ROD 04-JUN-1996 |
| LOCUS      | Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.  |        |        |                 |
| DEFINITION | L20957  |        |        |                 |
| ACCESSION  | L20957.1  |        |        |                 |
| VERSION    | GI:309348   |        |        |                 |
| KEYWORDS   | V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene. |        |        |                 |
| SOURCE     | Mus musculus (house mouse)  |        |        |                 |

|           |                     |  |  |
|-----------|---------------------|--|--|
| REFERENCE | JOURNAL             | 24 (11), 2874-2881 (1994)                                  |  |
| AUTHORS   | MEDLINE             | 95045941   |  |
| TITLE     | PUBMED              | 7957578  |  |
|           | 2 (bases 1 to 402)  |  |  |
| AUTHORS   | JOURNAL             | Iwasaki, Y., Takabatake, H., Monestier, M. and Ferrone, S. |  |
| TITLE     | MEDLINE             | 95331832   |  |
|           | PUBMED              | 7607710  |  |
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| Best Local Similarity | 89.8%; | Pred. No.    | 1.4e-100;     |             |                    |                           |                         |
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|                       |        |              |               |             |                    |                           |                         |
| Db                    | 1      | ATGAGAGT     | CTGAT         | CTTTTGTG    | CGTGTTCACAG        | CGCTTCCCTGGTCT            | CTCTGTCTGATGTG 60       |
|                       |        |              |               |             |                    |                           |                         |
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|                       |        |              |               |             |                    |                           |                         |
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|                       |        |              |               |             |                    |                           |                         |
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|                       |        |              |               |             |                    |                           |                         |
| Db                    | 121    | ACTGT        | CAC           | TGGCTACT    | CAATCACAG          | TGATATGCTCGGAACTGGAT      | CCGGCAGTTTCCA 180       |
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|            |   |           |           |                 |
|------------|---|-----------|-----------|-----------------|
| RESULT 11  | MUSIGHDOB   | 399 bp    | linear    | ROD 04-JUN-1996 |
| MUSIGHDOB  | Mus musculus Ig rearranged H-chain mRNA   |           |           |                 |
| LOCUS      | Mus musculus V-region, 5' end of cds.   |           |           |                 |
| DEFINITION | L20962  |           |           |                 |
| ACCESSION  | L20962.1  | GI:309346 |           |                 |
| VERSION    | V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene.   |           |           |                 |
| KEYWORDS   | Mus musculus (house mouse)  |           |           |                 |
| SOURCE     | Mus musculus  |           |           |                 |
| ORGANISM   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 399) |           |           |                 |
| REFERENCE  | Iwasaki.Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.   |           |           |                 |
| AUTHORS    | Structural profile of idiotype, anti-idiotypic and  |           |           |                 |
| TITLE      | anti-anti-idiotypic monoclonal antibodies in the HLA-DQ3 antigenic system   |           |           |                 |
| JOURNAL    | Eur. J. Immunol.  | 24 (11),  | 2874-2881 | (1994)          |
| MEDLINE    | 95045941  |           |           |                 |
| PUBMED     | 7957578   |           |           |                 |

REFERENCE 2 (bases 1 to 399)  
AUTHORS Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S.  
TITLE Idiotypic diversity and variable region gene usage by mouse  
anti-HLA-DQ3 mAb  
JOURNAL Immunogenetics 42 (2), 90-100 (1995)  
MEDLINE 95331832  
PUBMED 7607710  
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LOCUS MMU05284 417 bp mRNA linear ROD 31-JAN-1996  
DEFINITION Mus musculus BALB/c/J immunoglobulin heavy chain complete variable  
region (Igh) mRNA, partial cds.  
ACCESSION U05284

U05284.1 GI:463457  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 417)  
Tempest,P.R., White,P., Buttle,M., Carr,F.J. and Harris,W.J.  
Identification of framework residues required to restore antigen  
binding during reshaping of a monoclonal antibody against the  
glycoprotein gB of human cytomegalovirus  
Int. J. Biol. Macromol. 17 (1), 37-42 (1995)  
95290446  
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2 (bases 1 to 417)  
Tempest,P.R.  
Direct Submission  
Submitted (21-JAN-1994) Philip R. Tempest, ICOS Corporation, 22021  
20th Ave SE, Bothell, WA 98021, USA  
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DEFINITION Sequence 5 from Patent WO0043774.  
VERSION AX027688  
KEYWORDS AX027688.1 GI:10188558  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eshhar,Z. and Willner,I.  
TITLE Detection of small molecules by use of a piezoelectric sensor  
JOURNAL Patent: WO 0043774-A 5 27-JUL-2000;  
YISSUM RES DEV CO (IL); ESHHAR ZELIG (IL); WILLNER ITAMAR (IL);  
YEDA RES & DEV (IL)

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RESULT 14  
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LOCUS  
DEFINITION Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.  
1517 bp mRNA linear ROD 28-AUG-1996  
MMU65534  
Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.

ACCESSION U65534  
VERSION U65534.1 GI:1513181  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Xiao,X.W. and Frenkel,M.J.  
TITLE Full-length immunoglobulin gamma chain  
JOURNAL Unpublished  
AUTHORS Xiao,X.W. and Frenkel,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal  
Parade, Parkville, Victoria 3052, Australia

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RESULT 15  
SCU65536  
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DEFINITION Synthetic Mus musculus single chain Fv antibody precursor mRNA, complete cds.  
825 bp mRNA linear SYN 07-MAR-2000  
SCU65536  
Synthetic Mus musculus single chain Fv antibody precursor mRNA, complete cds.

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ACCESSION U65536 GI:1513185
VERSION U65536.1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 825)
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Single chain Fv with signal sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 825)
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal
Parade, Parkville, Victoria 3052, Australia
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: gb ba.\*
- 2: gb htg.\*
- 3: gb in.\*
- 4: gb om.\*
- 5: gb ov.\*
- 6: gb pat.\*
- 7: gb ph.\*
- 8: gb pl.\*
- 9: gb pr.\*
- 10: gb ro.\*
- 11: gb sts.\*
- 12: gb sy.\*
- 13: gb un.\*
- 14: gb vi.\*
- 15: em ba.\*
- 16: em fun.\*
- 17: em hum.\*
- 18: em in.\*
- 19: em mu.\*
- 20: em om.\*
- 21: em or.\*
- 22: em ov.\*
- 23: em pat.\*
- 24: em ph.\*
- 25: em pl.\*
- 26: em ro.\*
- 27: em sts.\*
- 28: em un.\*
- 29: em vi.\*
- 30: em htg hum.\*
- 31: em htg inv.\*
- 32: em htg other.\*
- 33: em htg mus.\*
- 34: em htg pin.\*
- 35: em htg rod.\*
- 36: em htg mam.\*
- 37: em htg virt.\*
- 38: em sy.\*
- 39: em htgo hum.\*
- 40: em htgo mus.\*
- 41: em htgo other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 381   | 100.0       | 381    | 6     | AR024275 Sequence  |
| 2          | 381   | 100.0       | 381    | 6     | AR045128 Sequence  |
| 3          | 381   | 100.0       | 381    | 6     | BD011352 Chimeric  |
| 4          | 381   | 100.0       | 381    | 6     | E05353 DNA encodin |
| 5          | 381   | 100.0       | 381    | 6     | E43822 Chimeric an |
| 6          | 381   | 100.0       | 381    | 6     | E05419 cDNA sequen |
| 7          | 359.2 | 94.3        | 381    | 10    | S50261 Ig VL=anti- |
| 8          | 359.2 | 94.3        | 381    | 6     | I33380 Sequence 1  |
| 9          | 359.2 | 94.3        | 381    | 10    | MUSIVJR            |
| 10         | 357.6 | 93.9        | 381    | 10    | MUSIGRAAL          |
| 11         | 356   | 93.4        | 381    | 10    | MMU16689           |
| 12         | 355.2 | 93.2        | 378    | 10    | AF045496           |
| 13         | 351.2 | 92.2        | 381    | 6     | AR016717 Sequence  |
| 14         | 351.2 | 92.2        | 381    | 10    | MMU05217           |
| 15         | 351.2 | 92.2        | 972    | 10    | AF466770 Mus muscu |
| 16         | 349.8 | 91.8        | 378    | 10    | MUSIGK527A         |
| 17         | 349.6 | 91.8        | 959    | 10    | BC015292           |
| 18         | 348.6 | 91.5        | 381    | 6     | A51499             |
| 19         | 348.6 | 91.5        | 381    | 6     | AR085777 Sequence  |
| 20         | 346.4 | 90.9        | 381    | 6     | AR024279           |
| 21         | 346.4 | 90.9        | 381    | 6     | AR045132 Sequence  |
| 22         | 346.4 | 90.9        | 381    | 6     | BD011356 Chimeric  |
| 23         | 346.4 | 90.9        | 381    | 6     | E05357 DNA encodin |
| 24         | 346.4 | 90.9        | 381    | 6     | E43826 Chimeric an |
| 25         | 346.4 | 90.9        | 381    | 6     | E05423 cDNA sequen |
| 26         | 341.2 | 89.6        | 366    | 10    | MUSIGCKO           |
| 27         | 338.4 | 88.8        | 382    | 6     | AR301133 Sequence  |
| 28         | 337   | 88.5        | 399    | 10    | AY081858 Mus muscu |
| 29         | 332.6 | 87.3        | 372    | 6     | E06647 cDNA encodi |
| 30         | 330   | 86.6        | 345    | 10    | MUSIGKCPW          |
| 31         | 328.8 | 86.3        | 395    | 10    | MUSIGRAAM          |
| 32         | 324   | 85.0        | 1019   | 10    | BC027418 Mus muscu |
| 33         | 322.4 | 84.6        | 408    | 6     | AR06747 Sequence   |
| 34         | 322.4 | 84.6        | 408    | 6     | AR032023 Sequence  |
| 35         | 322.4 | 84.6        | 408    | 6     | AR038519 Sequence  |
| 36         | 322.4 | 84.6        | 408    | 6     | AR267246 Sequence  |
| 37         | 322.4 | 84.6        | 408    | 6     | E05888 cDNA encodi |
| 38         | 322.4 | 84.6        | 408    | 10    | S63022 anti-gangli |
| 39         | 320.8 | 84.2        | 408    | 6     | AR050865 Sequence  |
| 40         | 320.8 | 84.2        | 408    | 6     | AR219876 Sequence  |
| 41         | 320.8 | 84.2        | 408    | 6     | E07922 cDNA encodi |
| 42         | 312   | 81.9        | 324    | 10    | MMIGKL229          |
| 43         | 312   | 81.9        | 324    | 10    | MMIGKL233          |
| 44         | 312   | 81.9        | 324    | 10    | MMIGKL38           |
| 45         | 312   | 81.9        | 324    | 10    | MUSIGKAVD          |

ALIGNMENTS

|            |   |                                     |        |     |        |                 |
|------------|---|-------------------------------------|--------|-----|--------|-----------------|
| RESULT 1   | AR024275  | Sequence 28 from patent US 5795965. | 381 bp | DNA | linear | PAT 05-DEC-1998 |
| LOCUS      | AR024275  | Sequence 28 from patent US 5795965. |        |     |        |                 |
| DEFINITION | AR024275  | Sequence 28 from patent US 5795965. |        |     |        |                 |
| ACCESSION  | AR024275  | Sequence 28 from patent US 5795965. |        |     |        |                 |
| VERSION    | AR024275.1  | GI:3977569                          |        |     |        |                 |
| KEYWORDS   | Unknown.  |                                     |        |     |        |                 |
| SOURCE     | Unknown.  |                                     |        |     |        |                 |
| ORGANISM   | Unclassified.   |                                     |        |     |        |                 |
| REFERENCE  | 1 (bases 1 to 381)  |                                     |        |     |        |                 |
| AUTHORS    | tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.William. |                                     |        |     |        |                 |
| TITLE      | Reshaped human to human interleukin-6 receptor                                    |                                     |        |     |        |                 |
| JOURNAL    | Patent: US 5795965-A 28 18-AUG-1998;  |                                     |        |     |        |                 |



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Db      241  AGGTTGAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCAA 300
Qy      301  GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360
Db      301  GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360
Qy      361  GGGACCAAGCTGGAATAAAT 381
Db      361  GGGACCAAGCTGGAATAAAT 381

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## RESULT 4

E05353  
LOCUS E05353 381 bp RNA linear PAT 29-SEP-1997  
DEFINITION DNA encoding v region of L chain of mouse monoclonal antibody against human interleukin-6 receptor.

ACCESSION E05353  
VERSION E05353.1 GI:2173542  
KEYWORDS JP 1993227970-A/3.

SOURCE Mus sp.  
ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 381)  
AUTHORS Tsuchiya M., Sato I., Mearii M.B., Suteilibun T.J. and Hose U.S.  
TITLE RECONSTRUCTED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR

JOURNAL Patent: JP 1993227970-A 3 07-SEP-1993;  
CHUGAI PHARMACEUT CO LTD

COMMENT OS Mus sp. (mouse)  
PN JP 1993227970-A/3  
PD 07-SEP-1993  
PF 19-FEB-1992 JP 1992032084

PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAGARETSUTO BENDEITSUGU,  
SUTERIBUN TAREN JIYONZU, HOSE UIRIAMU SARUDANA PC  
C12N15/13, C07K15/06, C12N15/10, C12P21/08, C12Q1/68//C07K15/28, PC  
C12N5/20.

PC C12N15/06, (C12P21/08, C12R1:91);

CC strandedness: Double;

CC topology: Linear;

CC \*source: clone=pPM-k3;

FT Key Location/Qualifiers

FT sig\_peptide 1..60

FT mat\_peptide 61..381.

FT Location/Qualifiers

1..381

/organism="Mus sp."

/mol\_type="genomic RNA"

/db\_xref="taxon:10095"

BASE COUNT 106 a 94 c 84 g 97 t

## ORIGIN

Query Match 100.0%; Score 381; DB 6; Length 381;  
Best Local Similarity 100.0%; Pred. No. 7.2e-114;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 60

Db 1 ATGGTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 60

Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGTCTGCTCTCTGGAGACAGAGTCAAC 120

Db 61 GATATCCAGATGACACAGACTACATCTCCCTGTCTGCTCTCTGGAGACAGAGTCAAC 120

Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180

Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180

Qy 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240

Db 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240

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Db 241 AGGTTGAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCAA 300

Qy 301 GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360

Db 301 GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360

Qy 361 GGGACCAAGCTGGAATAAAT 381

Db 361 GGGACCAAGCTGGAATAAAT 381

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Qy      121  ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180
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Qy      181  GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
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Db      241  AGGTTGAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCAA 300
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Db      301  GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360
Qy      361  GGGACCAAGCTGGAATAAAT 381
Db      361  GGGACCAAGCTGGAATAAAT 381

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## RESULT 5

E43822  
LOCUS E43822 381 bp DNA linear PAT 31-JAN-2002  
DEFINITION Chimeric antibody against human interleukin-6 receptor.

ACCESSION E43822  
VERSION E43822.1 GI:18627755  
KEYWORDS JP 2000116391-A/26.

SOURCE Mus sp.  
ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 381)  
AUTHORS Tsuchiya M., Sato I., Margaret B.M., Taren J.S. and William S.H.  
TITLE Chimeric antibody against human interleukin-6 receptor

JOURNAL Patent: JP 2000116391-A 26-APR-2000;  
CHUGAI PHARMACEUT CO LTD

COMMENT OS Mus sp. (mouse)  
PN JP 2000116391-A/26  
PD 25-APR-2000  
PF 29-NOV-1999 JP 1999338286

PI MASAYUKI TSUCHIYA, ISAO SATO, BENDIGGU MARY MARGARET, PI JONES  
STEVEN TAREN,  
PI SARUDANA HOSE WILLIAM

PC C12N15/09, C07K16/18, C07K16/26, C07K19/00, C12N5/10, C12P21/08, PC  
C12N15/00,

CC C12N5/00

CC C12N5/00

FT Key Location/Qualifiers

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FT mat\_peptide (61)..(381).

FT Location/Qualifiers

1..381

/organism="Mus sp."

/mol\_type="genomic DNA"

/db\_xref="taxon:10095"

BASE COUNT 106 a 94 c 84 g 97 t

## ORIGIN

Query Match 100.0%; Score 381; DB 6; Length 381;  
Best Local Similarity 100.0%; Pred. No. 7.2e-114;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 60

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Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGTCTGCTCTCTGGAGACAGAGTCAAC 120

Db 61 GATATCCAGATGACACAGACTACATCTCCCTGTCTGCTCTCTGGAGACAGAGTCAAC 120

Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180

Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180

Qy 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240

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Qy 241 AGGTTGAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCAA 300

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Qy 301 GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360

Db 301 GAAGACATTGCCACTTACTTTGGCAACAGGTTAAACAGGTTCCGTTACAGTTTCGGAGGG 360

Qy 361 GGGACCAAGCTGGAATAAAT 381

Db 361 GGGACCAAGCTGGAATAAAT 381

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Qy      241 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Db      241 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Qy      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
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Qy      361 GGGACCAAGCTGGAATAAAT 381
Db      361 GGGACCAAGCTGGAATAAAT 381
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RESULT 6
E05419
LOCUS   E05419          387 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION
cdna sequence encoding mouse monoclonal antibody kappa type L chain
variable region against human IL-6 receptor.
ACCESSION E05419
VERSION   E05419.1 GI:2173608
KEYWORDS  JP 1993236966-A/26.
SOURCE    Mus musculus
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 387)
Tsuchiya, M., Sato, I., Mearii, M.B. and Suteibun, T.J.
DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY
TO HUMAN INTERLEUKIN-6 RECEPTOR
Patent: JP 1993236966-A 26 17-SEP-1993;
CHUGAI PHARMACEUT CO LTD
OS (mouse)
PN JP 1993236966-A/26
PD 17-SEP-1993
PF 25-APR-1991 JP 1991095476
PI TSUCHIYA MASA YUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU,
PI SUTEIBUN TAREN JIYOONZU
PC C12N15/13//C12P21/08;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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CC *source: cell_lines=PMI;
CC *source: clone=ppm-k3;
Key      Location/Qualifiers
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FT      mat_peptide      61..387
FT      L chain
FT      variable region against human IL-6 receptor
FT      mature peptide'.
Location/Qualifiers
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BASE COUNT 106 a 87 g 98 t
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Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
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Db      1 ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
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Db      121 ATCAGTTGCGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGTTATCAGCAGAAACCA 180
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Db      241 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Qy      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
Db      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
Qy      361 GGGACCAAGCTGGAATAAAT 381
Db      361 GGGACCAAGCTGGAATAAAT 381
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RESULT 7  
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LOCUS S50261 381 bp mRNA linear ROD 08-MAY-1993  
DEFINITION  
Ig VL-anti-CD4 mAb M-T151 variable region light chain (J2, chimeric antibody) [mice, hybridoma cells, mRNA Partial, 381 nt].  
ACCESSION S50261  
VERSION S50261.1 GI:260761  
KEYWORDS Mus sp.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 381)  
Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C.,  
Flieger, D., Lenz, H., Weiss, E.H., Rieber, E.P., Riehmuller, G. et al.  
Combinatorial functions of two chimeric antibodies directed to  
human CD4 and one directed to the alpha-chain of the human  
interleukin-2 receptor  
Gene 121 (2), 271-278 (1992)  
93077041  
1446824  
PUBMED  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibseq 119499] from the original journal article.  
This sequence comes from Fig. 1a.  
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BASE COUNT 105 a 92 c 83 g 101 t

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ORIGIN
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Best Local Similarity 96.6%; Pred. No. 1.1e-106;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGCTCTGCTCTCTGGAGACAGAGTCAACC 120
Db 61 GATATCCAGATGACACAGACTATATCTCCCTCTCTGCTCTCTGGAGACAGAGTCAACC 120
Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGTTATTAAGTCGTATCAGCAGAAACCA 180
Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAACAAATTATTAAAGTCGTATCAGCAGAAACCA 180
Qy 181 GATGGAACCTATAAATCTCTGATCTATACATCAAGATTACACTCAGGAGTCCCATCA 240
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Qy 241 AGGTTCAAGTCAGTGGTCTGGAACAGATTATTCTCTCACCATTAAACCTGGAGCAA 300
Db 241 AGGTTCAAGTCAGTGGTCTGGAACAGATTATTCTCTCACCATTAAACCTGGAGCAA 300
Qy 301 GAAGACATTTGCCACTTACTTTTGCCAAACAGGGTAACACGCTTCGGTACACGTTCCGAGGG 360
Db 301 GAAGATGTTGCCACTTACTTTTGCCAAACAGGGTAATAGCTTCGGTACACGTTCCGAGGG 360
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 8
133380
LOCUS
DEFINITION
Sequence 1 from patent US 5591629.
ACCESSION
133380
VERSION
133380.1 GI:1824171
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 393)
AUTHORS
Rodriguez,M. and Miller,D.J.
TITLE
Monoclonal antibodies which promote central nervous system
remyelination
JOURNAL
Patent: US 5591629-A 1 07-JAN-1997;
FEATURES
Location/Qualifiers
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Query Match          94.3%; Score 359.2; DB 6; Length 393;
Best Local Similarity 96.6%; Pred. No. 1.1e-106;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTGCTCTGTTTCAAGGTACAGATGT 60
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Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAACAAATTATTAAAGTCGTATCAGCAGAAACCA 180
Qy 181 GATGGAACCTATAAATCTCTGATCTATACATCAAGATTACACTCAGGAGTCCCATCA 240
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ORIGIN
Query Match          94.3%; Score 359.2; DB 10; Length 381;
Best Local Similarity 96.6%; Pred. No. 1.1e-106;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 241 AGGTTCAAGTCAGTGGTCTGGAACAGATTATTCTCTCACCATTAAACCTGGAGGG 360
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Qy 361 GGGACCAAGCTGGAATAAA 380
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 9
MUSIVJR
LOCUS
DEFINITION
Mus musculus germline immunoglobulin light chain variable region
and joining region mRNA, 5' end.
ACCESSION
L35316
VERSION
L35316.1 GI:829182
KEYWORDS
germline; immunoglobulin light chain; joining region; variable
region.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 393)
AUTHORS
Miller,D.J. and Rodriguez,M.
TITLE
A monoclonal autoantibody that promotes central nervous system
remyelination in a model of multiple sclerosis is a natural
autoantibody encoded by germline immunoglobulin genes
JOURNAL
J. Immunol. 154 (5), 2460-2469 (1995)
MEDLINE
95173452
PUBMED
7868912
COMMENT
On May 24, 1995 this sequence version replaced gi:529425.
Original source text: Mus musculus (strain SJL/J) hyperimmunized
spleen mRNA.
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Location/Qualifiers
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Db 361 GGGACCAAGCTGGAATAAA 380

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DB 361 GGCACCAAGCTGGAAATAAA 380

RESULT 12  
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LOCUS 378 bp mRNA linear ROD 28-FEB-1998  
DEFINITION Mus musculus dc7 anti-poly(dC) monoclonal antibody kappa light chain variable region, (Igk) mRNA, partial cds.  
ACCESSION AF045496  
VERSION AF045496.1 GI:2906075  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 378)  
REFERENCE O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.  
AUTHORS Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies  
TITLE Unpublished  
JOURNAL

REFERENCE 2 (bases 1 to 378)  
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.  
AUTHORS Direct Submission  
TITLE JOURNAL  
SUBMITTED (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA  
FEATURES Location/Qualifiers  
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Matches 363; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
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DB 2 TGTCTCTCTGCTCAGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGTGATA 61  
QY 65 TCCAGATGACACAGACTACATCTCTGCTCTGCTCTCTGGGAGACAGAGTCAACATCA 124  
DB 62 TCCAGATGACGAGACTCCATCTCTGCTCTCTGGGAGACAGAGTCAACATCA 121  
QY 125 GTTTCAGGGCAAGTCAGGACATTAGCAGTTATTATAAATCTGGTATCAGCAGAAACCATG 184  
DB 122 GTTTCAGGGCAGTCAGGACATTAGCAATATTATTAACCTGGTATCAGCAGAAACCATG 181  
QY 185 GAACTATTAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGT 244  
DB 182 GAACTGTATAACTCCTGGTCTACTACACATCAAGATTAGCAATTTCAAGGTCCCATCAAGGG 241  
QY 245 TCAGTGGCAGTGGTCTGGAACAGATTATTCTCTCACCATTAACTGGAGCAAGAAG 304  
DB 242 TCAGTGGCAGTGGTCTGGAACAGATTATTCTCTCACCATTAGCACTGGAGCAAGAAG 301  
QY 305 ACATTGCCACTTACTTTTGGCAACAGGTTAACACGTTCCGTTACAGTTCGGAGGGGGGA 364  
DB 302 ATATTGCCACTTACTTTTGGCAACAGGTTAACTGCTTCGTTCCGTACACCTTCGGAGGGGGGA 361  
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DB 362 CCAAGCTGGAAATAAA 377  
RESULT 13  
AR016717  
LOCUS 381 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 4 from patent US 5777085.  
ACCESSION AR016717

Submitted (09-JAN-2002) Department of Biological Sciences,  
University of Ulsan, Ulsan 680-749, Korea



Search completed: October 24, 2003, 04:50:09  
Job time : 1526.09 secs

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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 02:25:30 ; Search time 189.538 Seconds  
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Title: US-09-114-285a-28  
Perfect score: 381  
Sequence: 1 AUGGTGCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 1          | 381   | 100.0       | 381    | 13 | AAQ30755 pPM-k3. Synthetic   |
| 2          | 359.2 | 94.3        | 381    | 14 | AAQ36607 Anti-CD4 antibody   |
| 3          | 359.2 | 94.3        | 393    | 16 | AAQ05311 MAB SCH94.03 light  |
| 4          | 351.2 | 92.2        | 381    | 14 | AAQ45662 Mouse C4G1 Ig light |
| 5          | 351.2 | 92.2        | 381    | 19 | AAV36741 Variable region of  |
| 6          | 349.6 | 91.8        | 381    | 18 | AAV59500 Mouse anti-human F  |
| 7          | 349.6 | 91.8        | 381    | 19 | AAV34426 Mouse antibody F91  |
| 8          | 348.6 | 91.5        | 381    | 17 | AAT35050 MAB VL17E6 light c  |

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| 9  | 348   | 91.3 | 444  | 11 | AAQ08608 ME4 Light Chain V   |
| 10 | 348   | 91.3 | 444  | 18 | AAT43440 MAB ME4 light chain |
| 11 | 348   | 91.3 | 444  | 20 | AAV71158 Coding strand for   |
| 12 | 348   | 91.3 | 444  | 25 | ABX79238 DNA encoding mouse  |
| 13 | 343.2 | 90.1 | 381  | 13 | AAQ30759 p146-k3. Synthe     |
| 14 | 338.4 | 88.8 | 382  | 18 | AAT73611 CDNA encoding light |
| 15 | 333.6 | 87.6 | 402  | 12 | AAQ12061 Sequence encoding   |
| 16 | 333.6 | 87.6 | 402  | 12 | AAQ12017 Sequence encoding   |
| 17 | 332.6 | 87.3 | 372  | 15 | AAQ56067 Murine immunoglob   |
| 18 | 322.4 | 84.6 | 408  | 21 | AAQ51004 Human IL-1 chimer   |
| 19 | 320.8 | 84.2 | 408  | 20 | AAQ99481 pKM641 LA2 immunog  |
| 20 | 319.2 | 83.8 | 408  | 14 | AAQ37058 Rat immunoglobulin  |
| 21 | 319.2 | 83.8 | 408  | 15 | AAQ45438 KM641 H chain vari  |
| 22 | 309.6 | 81.3 | 382  | 18 | AAT73656 CDNA for humanise   |
| 23 | 304.8 | 80.0 | 382  | 18 | AAT73652 CDNA for humanise   |
| 24 | 302.4 | 79.4 | 321  | 25 | ABT14041 Ganglioside-associ  |
| 25 | 301.6 | 79.2 | 382  | 18 | AAT73631 CDNA for humanise   |
| 26 | 301.6 | 79.2 | 382  | 18 | AAT73647 CDNA for humanise   |
| 27 | 300   | 78.7 | 382  | 18 | AAT73644 CDNA for humanise   |
| 28 | 299.2 | 78.5 | 324  | 16 | AAT05313 B-cell lymphoma CH  |
| 29 | 298.2 | 78.3 | 1931 | 25 | ABV73341 anti-CD22 monoclon  |
| 30 | 296   | 77.7 | 321  | 19 | AAV07641 anti-CD22 monoclon  |
| 31 | 295.2 | 77.5 | 1668 | 22 | AAAB9071 Activating polypep  |
| 32 | 295.2 | 77.5 | 1898 | 22 | AAAB9073 Activating polypep  |
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| 34 | 295.2 | 77.5 | 2115 | 22 | AAAB9088 MLV envelope glyco  |
| 35 | 294.4 | 77.3 | 324  | 21 | AAA27323 Murine consensus 1  |
| 36 | 292.2 | 76.7 | 702  | 22 | AAC91015 Chimeric 4H6 anti-  |
| 37 | 292.2 | 76.7 | 702  | 22 | AAC91016 Chimeric 4H6 anti-  |
| 38 | 289.8 | 76.1 | 1943 | 24 | ABK13467 DNA encoding immun  |
| 39 | 289.6 | 76.0 | 324  | 21 | AAQ01185 Murine monoclonal   |
| 40 | 289.6 | 76.0 | 324  | 21 | AAZ39345 Murine anti-integr  |
| 41 | 288.2 | 75.6 | 913  | 15 | AAQ81076 Bispecific CD3-L6F  |
| 42 | 288   | 75.6 | 1803 | 21 | AAAS8773 DNA encoding an im  |
| 43 | 288   | 75.6 | 1944 | 25 | ABX14413 DNA encoding recom  |
| 44 | 287.2 | 75.4 | 2023 | 25 | ABZ75116 Anti-human seminal  |
| 45 | 287.2 | 75.4 | 2952 | 24 | ABK13464 DNA encoding immun  |

ALIGNMENTS

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AAQ30755  
ID AAQ30755 standard; cDNA; 381 BP.

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| XX | AAQ30755;   |
| AC | AAQ30755;   |
| XX | 25-MAR-2003 (updated)   |
| DT | 30-MAR-1993 (first entry)   |
| XX | pPM-k3.   |
| XX | Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; |
| KW | heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;    |
| KW | plasmid; pPM-k3; pPM-h1; ss.  |
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| OS | Synthetic.  |
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| FT | /*tag= b  |
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| PN | 12-NOV-1992.  |
| XX | 24-APR-1992;  |
| XX | 92WO-JP00544.   |
| XX | 25-APR-1991;  |
| PR | 91JP-0095476.   |
| PR | 19-FEB-1992;  |
| PR | 92JP-0032084.   |



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QY 361 GGGACCAAGCTGGAAATAAA 380
DB 361 GGGACCAAGCTGGAAATAAA 380

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AAT05311
ID AAT05311 standard; DNA; 393 BP.
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AC AAT05311;
XX
XX 02-FEB-1996 (first entry)
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XX MAb SCH94.03 light chain DNA.
XX
XX Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system;
KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
KW ds.
XX
XX Mus sp.
XX
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XX FT 1..60
XX FT /*tag= b
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XX FT /*tag= c
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XX WO9530004-A1.
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XX 09-NOV-1995.
XX
XX 27-APR-1995; 95WO-US05262.
XX
XX 29-APR-1994; 94US-0236520.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Miller DJ, Rodriguez M;
XX WPI; 1995-393077/50.
XX P-PSDB; AAR84553.
XX
XX Monoclonal antibodies which stimulate central nervous system
XX re-myelination - are produced by hybridoma ATCC CRL 11627, for
XX treating multiple sclerosis, and viral or post-neural diseases of
XX the CNS.
XX
XX Disclosure; Page 36; 63pp; English.
XX
XX Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with
XX spinal cord homogenate from a mammal uninfected with any
XX demyelinating disease. The hybridoma produced a monoclonal antibody
XX (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
XX light chain germline sequence is given in AAT05311.
XX
XX Sequence 393 BP; 105 A; 96 C; 89 G; 103 T; 0 other;
XX
Query Match 94.3%; Score 359.2; DB 16; Length 393;
Best Local Similarity 96.6%; Pred. No. 5.8e-102;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGGTGCTCCTCAGCTCAGTTCCTGGTCTCCTGCTGCTCTCTTTTCAAGGTACCAGATGT 60
DB 1 ATGATGTCTCTGCTCAGTTCCTGGTCTCCTGCTGCTCTCTTTTCAAGGTACCAGATGT 60
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DB 61 GATATCCAGATGACACAGACTACATCCCTGCTGCTCTCTGGGAGACAGAGTACC 120
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361 GGCACCAAGCTGGAAATCAA 380

RESULT 4
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ID AAQ45662 standard; cDNA; 381 BP.
XX
XX AAQ45662;
XX
XX 25-MAR-2003 (updated)
XX 29-NOV-1993 (first entry)
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XX Mouse C4G1 Ig light-chain coding sequence.
XX
XX Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody; ss.
XX
XX Synthetic.
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XX WO9313133-A1.
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XX 08-JUL-1993.
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XX 15-DEC-1992; 92WO-JP01630.
XX
XX 20-DEC-1991; 91US-0812111.
XX 09-JUN-1992; 92US-0895952.
XX 11-SEP-1992; 92US-0944159.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX Co MS, Tso JY;
XX
XX WPI; 1993-227275/28.
XX P-PSDB; AAR39265.
XX
XX Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa
XX protein - for treating disorders related to vascular thrombosis
XX
XX Disclosure; Fig 2A; 54pp; Japanese.
XX
XX This sequence encodes the mouse C4G1 immunoglobulin light chain.
XX See AAQ45663 for the heavy-chain coding sequence. The antibody is
XX specific for the GPIIb/IIIb protein and inhibits platelet
XX agglutination. The Ig is thus useful in the treatment of
XX thrombosis.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX

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QY 61 GATATCCAGATGACACAGACTACATCTCTCCCTGTCTGCTCTCTCTGGGAGACAGAGTCACC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 ATCAGTTGCGAGGCAAGTCAGGACATTTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 ATCAGTTGCGAGGCAAGTCAGGACATTTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GATGAACTATTAAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GAAGACATTTGCCACTTACTTTTGGCCAAAGGGTAACAGCTTCCGTACACAGTTCCGAGGG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GGAGATATTGCCACTTACTTTTGGCCAAAGGGTAGTACGTTCCGTGGACGTTCCGTTGGA 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGGACCAAGCTGGAAATAAA 380
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGCACCAAGCTGGAAATCAA 380
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 8
AAT35050
ID AAT35050 standard; cDNA; 381 BP.
XX
AC AAT35050;
XX
DT 10-JAN-1997 (first entry)
XX
DE MAB VLI7E6 light chain (specific for human alphav integrins).
XX
KW Monoclonal antibody; MAb; integrin; cell-matrix interaction;
KW tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
KW imaging; detection; radiolabel; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT mat_peptide /*tag= a
FT mat_peptide 61..381
FT mat_peptide /*tag= b
XX
PN EP719859-A1.
XX
PD 03-JUL-1996.
XX
PF 06-DEC-1995; 95EP-0119233.
XX
PR 20-DEC-1994; 94EP-0120165.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;
PI Rosell E;
XX
DR WPI: 1996-302345/31.
DR P-PSDB; AAR99003.
XX
PT New human integrin V chain-specific monoclonal antibody - and
PT related DNA and hybridomas, for treatment and diagnostic imaging of
PT tumours, esp melanoma.
XX
PS Claim 14; Figure 17a; 54pp; English.
XX
CC A monoclonal antibody which reacts only with the alphav chain of
CC human alphav integrins; which blocks attachment of alphav integrin
CC bearing cells to integrin substrate; which reverses established cell
```

```
CC matrix interactions caused by alphav integrin; which blocks tumour
CC development and which has no cytotoxic activity, may be used to
CC treat tumours, especially melanoma (but also glioma, carcinoma)
CC optionally coupled to a cytokine such as interleukin-2. The
CC monoclonal antibody may also be used for diagnostic imaging of
CC tumours and assessment of tumour growth when conjugated to a
CC radiolabel or a radio opaque-agent.
XX
SQ Sequence 381 BP; 105 A; 88 C; 85 G; 103 T; 0 other;
```

```
Query Match 91.5%; Score 348.6; DB 17; Length 381;
Best Local Similarity 95.0%; Pred. No. 1.2e-98;
Matches 360; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 ATGTTGTCCTCAGTCTCAGTTCCTTGGTCTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GATATCCAGATGACACAGACTACATCTCTCCCTGTCTGCTCTCTGGGAGACAGAGTCACC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GATATCCAGATGACACAGACTACATCTCTCCCTGTCTGCTCTCTGGGAGACAGAGTCATC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 ATCAGTTGCGAGGCAAGTCAGGACATTTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 ATCAGTTGCGAGGCAAGTCAGGACATTTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GATGAACTATTAAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GATGAACTATTAAACTCTGATCTACTACACATCAAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 AGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GAAGACATTTGCCACTTACTTTTGGCCAAAGGGTAACAGCTTCCGTACACAGTTCCGAGGG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GAAGATATTGCCACTTACTTTTGGCCAAAGGGTAATAGTTTCCGTACACGTTCCGAGGG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGGACCAAGCTGGAAATAAA 379
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGCACCAAGCTGGAAATGA 379
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 9
AAQ08608
ID AAQ08608 standard; DNA; 444 BP.
XX
AC AAQ08608;
XX
DT 25-MAR-2003 (updated)
DT 04-MAR-1993 (first entry)
XX
DE ME4 Light Chain V Region (mouse).
XX
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 61..444
FT /*tag= a
XX
PN WO9002569-A.
XX
PD 22-MAR-1990.
XX
PF 06-SEP-1989; 89WO-US03852.
XX
PR 06-SEP-1988; 88US-0240624.
PR 08-SEP-1988; 88US-0241744.
PR 13-SEP-1988; 88US-0243739.
PR 04-OCT-1988; 88US-0253002.
```





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Db 241 GATGAACTGTTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 300
Qy 241 AGGTTCACTGGCAGTGGTCTGGAACAGATTATCTCTCACCATTAACAACCTGGAGCAA 300
Db 301 AGGTTCACTGGCAGTGGTCTGGAACAGATTATCTCTCACCATTAACAACCTGGAGCAA 360
Qy 301 GAAGACATTGCCACTTACTTTTGGCCACAGGGTAACACGCTTCCGTACACAGTTGGGAGGG 360
Db 361 GAAGATTGTCACCTTACTTTTGGCCACAGGGTAATATCTCTCGACCGTTCGGTGA 420
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 421 GGCACCAAACTGGAATCAA 440

```

## RESULT 11

AAV71158  
ID AAV71158 standard; DNA; 444 BP.

XX  
AC AAV71158;

DT 20-MAR-2003 (updated)  
DT 16-APR-1999 (first entry)

XX Coding strand for mouse ME4 light chain variable region.

XX Light chain variable region; murine antibody ME4; antibody ING-1;  
KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;  
KW treatment; human cancer; ss.

XX Mus sp.

FH Key Location/Qualifiers  
FT CDS 61..444  
/\*tag= a  
/note= "partial CDS, no termination codon"

PN US5843685-A.

XX 01-DEC-1998.

XX 06-JUN-1995; 95US-0466034.

XX 06-SEP-1989; 89WO-US03852.

XX 06-MAY-1991; 91US-0659401.

XX 27-DEC-1994; 94US-0364001.

XX 06-SEP-1988; 88US-0240624.

XX 08-SEP-1988; 88US-0241744.

XX 13-SEP-1988; 88US-0243739.

XX 04-OCT-1988; 88US-0253002.

XX 19-JUN-1989; 89US-0367641.

XX 21-JUL-1989; 89US-0382768.

XX (XOMA ) XOMA CORP.

XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;

XX WPI; 1999-044574/04.

XX P-PSDB; AAW85062.

XX Chimeric antibody specific for human tumour antigen - useful as

XX immunoassay, imaging or antitumour agent

XX Example 3; Fig 29; 92pp; English.

XX The present sequence encodes the light chain variable region of

XX murine antibody ME4. The sequence was used to create chimeric

XX mouse-human immunoglobulins which recognise the human tumour

CC antibody-dependent cellular cytotoxicity to target cells. The  
CC chimeric antibodies can be used for therapeutic purposes in the  
CC treatment of human cancer.  
CC (Updated on 20-MAR-2003 to correct PR field.)

XX Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 Other;

Qy Query Match 91.3%; Score 348; DB 20; Length 444;  
Best Local Similarity 94.7%; Pred. No. 1.9e-98;  
Matches 360; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGGTGTCTCCTCAGTCTCAGTTCCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACAGATGT 60  
Db 61 ATGATGTCTCTGCTCAGTTCCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACAGATGT 120

Qy 61 GATATCCAGATGACACAGACTACATCTCCTGCTGCTCTCTGGGAGACAGAGTCAACC 120  
Db 121 GATATCCAGATGACACAGACTACATCTCCTGCTGCTCTCTGGGAGACAGAGTCAACC 180

Qy 121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTTATTTAACTGGTATCAGCAAAACCA 180  
Db 181 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTTATTTAACTGGTATCAGCAAAACCA 240

Qy 181 GATGAACTATTAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 241 GATGAACTGTAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 300

Qy 241 AGGTTCACTGGCAGTGGTCTGGAACAGATTATTTCTCTCACCATTAAACAACCTGGAGCAA 300  
Db 301 AGGTTCACTGGCAGTGGTCTGGAACAGATTATTTCTCTCACCATTAGCAACCTGGAGCAA 360

Qy 301 GAAGACATTGCCACTTACTTTTGGCCACAGGGTAACACGCTTCCGTACACGTTCCGAGGG 360  
Db 361 GAAGATTGTCACCTTACTTTTGGCCACAGGGTAATATCTCTCGACCGTTCGGTGA 420

## RESULT 12

ABX79238  
ID ABX79238 standard; DNA; 444 BP.

XX AC ABX79238;

DT 16-APR-2003 (first entry)

XX DNA encoding mouse antibody light chain variable region #4.

XX Mouse; human tumour antigen; anti-human tumour antigen-antibody;  
KW ING-1 antibody; cell line HB9812; immunoassay; imaging;  
KW tumour diagnosis; tumour therapy; cytostatic; gene; ds;  
KW light chain variable region.

XX Mus sp.

XX US6461824-B1.

XX 08-OCT-2002.

XX 06-JUN-1995; 95US-0467142.

XX 06-SEP-1989; 89US-0659401.

XX 06-SEP-1989; 89WO-US03852.

XX 27-DEC-1994; 94US-0364001.

XX 06-SEP-1988; 88US-0240624.

XX 08-SEP-1988; 88US-0241744.

XX 13-SEP-1988; 88US-0243739.

XX 04-OCT-1988; 88US-0253002.

XX 19-JUN-1989; 89US-0367641.

XX 21-JUL-1989; 89US-0382768.

(XOMA ) XOMA TECHNOLOGY LTD.

Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

WPI; 2003-196707/19.

P-PSDB; ASU58896.

Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody -

Example 3; Fig 29; 101pp; English.

The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line HB9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunoassay method for detecting an antigen in a sample by contacting a label-detectable antigen in the sample with the antibody, detecting the label and relating the detected label to the presence of a label-detectable use in an imaging method for revealing the presence of a label-detectable antigen in an animal by contacting the antibody with a part of the animal suspected of containing the antigen, detecting the label and relating the detected label to the presence of the antigen; and for killing cells carrying an antigen by contacting the cells with the antibody and allowing the killing to occur. The antibodies are useful in tumour diagnosis and therapy. The chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues imply that these antibodies may mediate selective destruction of malignant tissue. The presence of human rather than murine antigenic determinants on the chimeric antibodies increases their resistance to rapid clearance from the body relative to the original murine mAbs. This resistance to clearance enhances the potential utility of these chimeric antibodies, as well as their derivatives, in tumour diagnosis and therapy. This sequence encodes a mouse antibody light chain variable region used in the creation of an anti-human tumour antigen-antibody.

Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;

```

Query Match          91.3%; Score 348; DB 25; Length 444;
Best Local Similarity 94.7%; Pred. No. 1.9e-98;
Matches 360; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGTCAGTTCCTGGTCTCCTGTTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
Db 61 ATGATGTCCTCTGCTCAGTTCCTGGTCTCCTGTTCTCTGTTTCAAGGTACCAGATGT 120

Qy 61 GATATCCAGATGACACAGACTACATCCTCCCTGCTGCTCTCTGGGAGACAGAGTACC 120
Db 121 GATATCCAGATGACACAGACTACATCCTCCCTGCTGCTCTCTGGGAGACAGAGTACC 180

Qy 121 ATCAGTTCCAGGGCAAGTCAGACATTAGCAGTTATTTAACTGGTATCAGCAAGAACCA 180
Db 191 ATCAGTTCCAGGGCAAGTCAGACATTAGCAGTTATTTAACTGGTATCAGCAAGAACCA 240

Qy 191 GATGGAACATTATAACTCCTGATCTACTACATCATCAGATTACACTCAGGAGTCCCATCA 240
Db 241 GATGGAACCTGTTAACTCCTGATCTACTACATCATCAGATTACACTCAGGAGTCCCATCA 300

Qy 241 AGGTTCAAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAACAACCTGGAGCA 300
Db 301 AGGTTCAAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAACAACCTGGAGCA 360

Qy 301 GAAGACATTGCCACTTACTTTTGGCAACAGGGTAACAGCTTCGGTACACCGTTGGAGGG 360
Db 361 GAAGATTTTGGCACTTACTTTTGGCAACAGGGTAATATATCTCTCGGACCGTTGGTGA 420

Qy 361 GGGACCAAGCTGGAAATAAA 380

```

Db 421 GGCACCAAACTGGAAATCAA 440

RESULT 13

AAQ30759  
ID AAQ30759 standard; cDNA; 381 BP.

XX AAQ30759;

AC AC

25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

XX DE

XX DE

XX DE

XX DE

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XX DE

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Search completed: October 24, 2003, 03:57:07  
Job time : 191.538 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:39:05 ; Search time 1673.61 Seconds  
(without alignments)  
5532.953 Million cell updates/sec

Title: US-09-114-285A-28

Perfect score: 381

Sequence: 1 ATGCTGCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_est3.\*

12: gb\_est4.\*

13: gb\_est5.\*

14: gb\_est6.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 339.4 | 89.1        | 1459   | 13 | BQ918407    |
| 2          | 338.6 | 88.9        | 827    | 12 | BI152061    |
| 3          | 336.8 | 88.4        | 669    | 10 | BF123422    |
| 4          | 327.2 | 85.9        | 830    | 12 | BI455041    |

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|----|-------|------|------|----|----------|
| 5  | 322.4 | 84.6 | 708  | 12 | BI103114 |
| 6  | 312   | 81.9 | 725  | 10 | BF580940 |
| 7  | 309.8 | 81.3 | 966  | 10 | BF578083 |
| 8  | 308.8 | 81.0 | 626  | 10 | BF582283 |
| 9  | 300.4 | 78.8 | 774  | 10 | BF123744 |
| 10 | 305.6 | 77.6 | 354  | 13 | BY235531 |
| 11 | 294.8 | 77.4 | 772  | 10 | BF581992 |
| 12 | 262.2 | 68.8 | 730  | 28 | AZ313441 |
| 13 | 250.4 | 65.7 | 714  | 12 | BG963548 |
| 14 | 242.4 | 63.6 | 762  | 14 | CB958057 |
| 15 | 242.4 | 63.6 | 888  | 13 | BO881840 |
| 16 | 242.4 | 63.6 | 920  | 13 | BU899295 |
| 17 | 240.8 | 63.2 | 493  | 9  | AW405753 |
| 18 | 240.8 | 63.2 | 554  | 14 | CB956317 |
| 19 | 240.8 | 63.2 | 793  | 14 | CB987506 |
| 20 | 240.8 | 63.2 | 1019 | 12 | BM914405 |
| 21 | 239.8 | 62.9 | 785  | 14 | CB986236 |
| 22 | 239.8 | 62.9 | 837  | 14 | CB984807 |
| 23 | 239.2 | 62.8 | 431  | 9  | AW406886 |
| 24 | 239.2 | 62.8 | 864  | 10 | BG548281 |
| 25 | 239.2 | 62.8 | 943  | 10 | BF976230 |
| 26 | 239.2 | 62.8 | 1100 | 10 | BF663472 |
| 27 | 237.6 | 62.4 | 447  | 9  | AW405752 |
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| 29 | 237.6 | 62.4 | 724  | 14 | CB959008 |
| 30 | 237.6 | 62.4 | 725  | 14 | CB987519 |
| 31 | 237.6 | 62.4 | 753  | 14 | CB955708 |
| 32 | 237.6 | 62.4 | 755  | 10 | BG533970 |
| 33 | 237.6 | 62.4 | 759  | 14 | CB986444 |
| 34 | 237.6 | 62.4 | 805  | 14 | CB955618 |
| 35 | 237.6 | 62.4 | 807  | 14 | CB958795 |
| 36 | 237.6 | 62.4 | 855  | 14 | CB995312 |
| 37 | 237.6 | 62.4 | 891  | 13 | BX336281 |
| 38 | 237.6 | 62.4 | 943  | 13 | BQ707106 |
| 39 | 237.6 | 62.4 | 964  | 13 | BQ706786 |
| 40 | 237.6 | 62.4 | 959  | 13 | BU899279 |
| 41 | 236.6 | 62.1 | 750  | 14 | CB956930 |
| 42 | 236.4 | 62.0 | 773  | 14 | CB956597 |
| 43 | 236   | 61.9 | 472  | 9  | AW406323 |
| 44 | 236   | 61.9 | 735  | 14 | CB957697 |
| 45 | 236   | 61.9 | 738  | 14 | CB987788 |

ALIGNMENTS

RESULT 1

BQ918407

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ918407. 1459 bp mRNA linear EST 20-AUG-2002  
AGENCOURT 8885602 NCI CGAP Co24 Mus musculus cDNA clone  
IMAGE:6397382 5', mRNA sequence.

BQ918407 GI:22333105

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

1 (bases 1 to 1459)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAMI3895 row: c column: 15

High quality sequence start: 165





| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
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| 62        | ...     | ...   | ...     | ...     |
| 63        | ...     | ...   | ...     | ...     |
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| 91        | ...     | ...   | ...     | ...     |
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| 95        | ...     | ...   | ...     | ...     |
| 96        | ...     | ...   | ...     | ...     |
| 97        | ...     | ...   | ...     | ...     |
| 98        | ...     | ...   | ...     | ...     |
| 99        | ...     | ...   | ...     | ...     |
| 100       | ...     | ...   | ...     | ...     |

| FEATURES              | SOURCE    |
|-----------------------|-----------|
| 1. <b>Feature 1</b>   | Source 1  |
| 2. <b>Feature 2</b>   | Source 2  |
| 3. <b>Feature 3</b>   | Source 3  |
| 4. <b>Feature 4</b>   | Source 4  |
| 5. <b>Feature 5</b>   | Source 5  |
| 6. <b>Feature 6</b>   | Source 6  |
| 7. <b>Feature 7</b>   | Source 7  |
| 8. <b>Feature 8</b>   | Source 8  |
| 9. <b>Feature 9</b>   | Source 9  |
| 10. <b>Feature 10</b> | Source 10 |

BASE COUNT  
ORIGIN

227 a 230 c 172 g 201 t

| Query Match           | 85.9%   | Score 327.2       | DB 12    | Length 830 |
|-----------------------|---|-------------------|----------|------------|
| Best Local Similarity | 91.3%   | Pred. No. 3.3e-90 |          |            |
| Matches 347           | Conservative 0  | Mismatches 33     | Indels 0 | Gaps 0     |
| Qy 1                  | ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT       | 60                |          |            |
| Db 6                  | ATGATGTCTCTGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTTCAGATGT        | 65                |          |            |
| Qy 61                 | GATATCCAGATGACAGACTACATCCTCCTGTCTGCTCTCTGGGAGACAGAGTCACC        | 120               |          |            |
| Db 66                 | GATATCCAGATGACCCAGACTACATCCTCCTGTCTGCTCTCTGGGGGACAGAGTCACC      | 125               |          |            |
| Qy 121                | ATCAGTTGCAGGCGAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA      | 180               |          |            |
| Db 126                | ATCAATTCGAGGCGAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA      | 185               |          |            |
| Qy 181                | GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA    | 240               |          |            |
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| Qy 241                | AGTTTCAGTGGGACAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA | 300               |          |            |
| Db 246                | AGGTTCACTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAACAACCTGGAAACGA  | 305               |          |            |
| Qy 301                | GAAGACATTGCCACTTTACTTTTCCCAACAGGGTAAACGCTTCGCTACACGTTCCGGAGGG   | 360               |          |            |
| Db 306                | GAAGATATTGCCACTTTACTTTTCCCAACAGGGTAAATTCGGCTTCTCTCACGTTCCGGTCT  | 365               |          |            |
| Qy 361                | GGGACCAAGCTGGAAATAAA  | 380               |          |            |
| Db 366                | GGGACCAAACTGGAACTGAA  | 385               |          |            |

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|------------|--|---|--------|
| 05         | 306  | GAGAGATATGCCACATACATTTTCCACACAGGAGTAATTCGGCTTCTCAGCTTCGGTGGCT | 368    |
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| Qy         | 361  | GGGACCAAGCTGGAAATAAA  | 380    |
|            |  |   |        |
| Db         | 366  | GGGACCAAACTGGAACTGAA  | 385    |
|            |  |   |        |
| RESULT 5   |  |   |        |
|            | Bi103114   | 708 bp  | linear |
| LOCUS      | Bi103114   | 708 bp  | mRNA   |
| DEFINITION | 602889345F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5044690 |   |        |
|            | 5', mRNA sequence.   |   |        |
| ACCESSION  | Bi103114   |   |        |



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RESULT 7
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LOCUS
DEFINITION 602094759p1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209015 5',
mRNA sequence.
ACCESSION BF578083
VERSION BF578083.1 GI:11651795
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9774 row: e column: 16
High quality sequence stop: 614.
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:4209015"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 277 a 276 c 205 g 208 t
ORIGIN
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Best Local Similarity 92.3%; Pred. No. 8.9e-85;
Matches 348; Conservative 0; Mismatches 27; Indels 2; Gaps 2;
Qy 3 GGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCATGTGA 62
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Db |||||
Qy 63 TATCCAGATGACACAGCTACATCTCCCTGCTGCTCTCTGGGAGACAGTCAACAT 122
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Qy 72 TATCCAGATGACACAGCTACATCTCCCTGCTGCTCTCTGGGAGACAGTCAACAT 131
Db |||||
Qy 123 CAGTTGACGGGCAAGTCAGGACATTAGCAGTATTATTAACCTGGGTATCAGCAGAAACAGA 182
Db |||||
Qy 132 CAGTTGACGGTCAAGTCAGGACATTAGCAATTATTAACCTGGGTATCAGCAGAAACCGGA 191
Db |||||
Qy 183 TGGAACTATTAACTCCTGATCTACTACATCATCAAGATTATCACTCAGGAGTCCCATCAAG 242
Db |||||
Qy 192 TGGAACTGTAACTCCTGATCTACTACATCATCAAGATTATCACTCAGGAGTCCCATCTAG 251
Db |||||
Qy 243 GTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTACCATTAACAACCTGGAGCAAGA 302
Db |||||
Qy 252 GTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTACCATTAACAACCTGGAGCAAGA 311
Db |||||
Qy 303 AGACATTGCCACTTACTTTTGCACAGGGTAACACGCTTCGGTACAGTTTCGAGGGGG 362
Db |||||
Qy 312 AGATA-TGCCACTTAC-TTGGCAACACGGTACTACCCCTCCGTTGGACGTTTGTGGAG 369
Db |||||
Qy 363 GACCAAGCTGGAATAAA 379
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Db 370 CACCAAGGTGGAAGTCA 386
RESULT 8
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LOCUS
DEFINITION 602101109f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224267 5',
mRNA sequence.
ACCESSION BF582283
VERSION BF582283.1 GI:11655995
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 626)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9814 row: a column: 04
High quality sequence stop: 624.
Location/Qualifiers
1..626
/organism="Mus musculus"
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/notes="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 178 a 153 c 137 g 158 t
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Best Local Similarity 90.0%; Pred. No. 1.5e-84;
Matches 342; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
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Db |||||
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Db |||||
Qy 60 GATATCCAGATGACACAGACTACATCTCCCTGCTCTCTCTGGGAGACAGAGTCAACC 119
Db |||||
Qy 121 ATCAGTTGCGGGCAAGTCAGGACATTAGCAGTATTATTAACCTGGTATCAGCAAAACCA 180
Db |||||
Qy 120 ATCAATTTGCAGTGCAGTCAGGCAATTAGCAATTTATTAATTTGTTATCAGCAAAACCA 179
Db |||||
Qy 181 GATGGAATATTAACTCCTGATCTACTACATCAAGATTATCACTCAGGAGTCCCATCA 240
Db |||||
Qy 180 GATGGAATATTAACTCCTGATCTACTACATCAAGATTATTAATTTGTTATCAGGAGTCCCATCA 239
Db |||||
Qy 241 AGGTTTCAAGTGGCAGTGGGTCTGGAACAGATTATTTCTCTCACCATTAAACCTGGAGCAA 300
Db |||||
Qy 240 AGGTTTCAAGTGGCAGTGGGTCTGGAACAGATTATTTCTCTCACCATTAAACCTGGAGCACT 299
Db |||||
Qy 301 GAAGACATTGCCACTTACTTTTTCGCAACAGGGTAACACGCTTCCGTCGATCACGTTTCGAGGG 360
Db |||||
Qy 300 GAAGATATTGCCACTTACTATTGTCAGCAGTATTTTAAAGCTTCCATTGACGCTCGGCTCG 359
Db |||||
```

—



JOURNAL  
COMMENT

plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0016 row: K column: 06  
Seq primer: CTTGTAAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 730.

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source

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/db\_xref="taxon:10090"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWP42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

Query Match 68.8%; Score 262.2; DB 28; Length 730;  
Best Local Similarity 90.9%; Pred. No. 4.6e-70;  
Matches 279; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 104 TCGGAGACAGTCCACATCAGTTCAGGCGAGTCAGACATTTAGCAGTTATTTAACT 163  
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QY 164 GGTATCAGCAGAAACACAGATGAACTATTTAACTCCTGATCTACTACATCAAGATTAC 223  
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QY 224 ACTCAGGAGTCCATCAAGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCACA 283  
DB 522 ACTCAGGAGTCCATCAAGGTTTCAGTGGCAGTGGGTCTGGGAGGAGATTATTTCTCACA 463

QY 284 TTAACAACCTGAGCAGAGACATTGCCACTTACTTTTGGCAACAGGGTAACAGCTTC 343  
DB 462 TCAGCAACCTGGAACCTGAAGATATTTGCCACTTACTTTTGGCAGGATAGTAAGCTTC 403

QY 344 CGTACAC 350  
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## Db 402 CTCAC 396

RESULT 13  
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LOCUS

DEFINITION BG963548 714 bp mRNA linear EST 12-JUN-2001  
602831226F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4985791 5',  
mRNA sequence.

ACCESSION BG963548  
VERSION BG963548.1 GI:14351185  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 714)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LIAM10994 row: c column: 08

High quality sequence stop: 712.

FEATURES  
source

1. .714

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/clone="IMAGE:4985791"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI\_CGAP\_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 189 a 178 c 167 g 180 t

## ORIGIN

Query Match 65.7%; Score 250.4; DB 12; Length 714;  
Best Local Similarity 78.7%; Pred. No. 2.1e-66;  
Matches 299; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

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DB 16 ATCAGGGCTCTGCTCAGTTTCTTGGCATCTTGTCTCTGTTTTCAGGTGCCAGATGT 75

QY 61 GATATCAGATGACACAGACTACATCTCCTGCTGCTCTCTGGGAGACAGAGTACC 120  
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QY 241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTTAACTTGGAGCAA 300  
DB 256 AGGTTTCAGTGGCAGTGGGTCTGGGTGAGTATTTCTCTCACCATCAGCAGCTAGAGTCT 315

QY 301 GAAGACATTTGCCATTTACTTTTGGCAACAGGGTAACAGCTTCCGTCACACGTTGGAGGG 360  
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[illegible]

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Db 76 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 135
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Db 136 ATCACTTGCGGGCGAGTCAGGACATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 195
Qy 181 GATGGAACCTATTAAACTCTGTATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
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Qy 241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
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Qy 301 GAAGACATTGCCACTTACTTTTGGCCAAACAGGGTAACAGCTTCCGTACACGTTGGAGGG 360
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Qy 361 GGGACCAAGCTGGAAATAAA 380
Db 376 GGGACCAAGTGGATATCAA 395

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Search completed: October 24, 2003, 05:48:28  
 Job time : 1680.61 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:51:21 ; Search time 53.8788 Seconds  
(without alignments)  
3121.209 Million cell updates/sec

Title: US-09-114-285A-28

Perfect score: 381

Sequence: 1 ATGGTGTCCCTCAGTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
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- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 1          | 381   | 100.0       | 381    | 1     | US-08-137-117D-28 |
| 2          | 381   | 100.0       | 381    | 1     | US-08-436-717-28  |
| 3          | 359.2 | 94.3        | 393    | 1     | US-08-236-520-1   |
| 4          | 359.2 | 94.3        | 393    | 5     | PCT-US95-05262-1  |
| 5          | 351.2 | 92.2        | 381    | 1     | US-08-458-516-4   |
| 6          | 348.6 | 91.5        | 381    | 2     | US-08-574-699A-1  |
| 7          | 346.4 | 90.9        | 381    | 1     | US-08-137-117D-36 |
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| 9          | 338.4 | 88.8        | 382    | 3     | US-08-836-561-28  |
| 10         | 338.4 | 88.8        | 382    | 4     | US-09-434-132-28  |
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| 13         | 322.4 | 84.6        | 408    | 2     | US-08-454-680-5   |
| 14         | 322.4 | 84.6        | 408    | 4     | US-09-225-322B-9  |
| 15         | 322.4 | 84.6        | 408    | 4     | US-09-764-304-9   |
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| 17         | 320.8 | 84.2        | 408    | 2     | US-08-438-562-19  |
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| 19         | 320.8 | 84.2        | 408    | 3     | US-08-673-799C-19 |
| 20         | 320.8 | 84.2        | 408    | 4     | US-09-393-385B-19 |
| 21         | 309.6 | 81.3        | 382    | 3     | US-08-836-561-102 |
| 22         | 309.6 | 81.3        | 382    | 4     | US-09-434-122-102 |
| 23         | 304.8 | 80.0        | 382    | 3     | US-08-836-561-97  |
| 24         | 304.8 | 80.0        | 382    | 4     | US-09-434-122-97  |
| 25         | 301.6 | 79.2        | 382    | 3     | US-08-836-561-70  |
| 26         | 301.6 | 79.2        | 382    | 3     | US-08-836-561-91  |
| 27         | 301.6 | 79.2        | 382    | 4     | US-09-434-122-70  |

Sequence 91, Appl  
Sequence 87, Appl  
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Sequence 3, Appl  
Sequence 9, Appl  
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Sequence 15, Appl  
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Sequence 16, Appl  
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Sequence 29, Appl  
Sequence 29, Appl  
Sequence 17, Appl

#### ALIGNMENTS

RESULT 1  
US-08-137-117D-28  
; Sequence 28, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid







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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 61..129
, OTHER INFORMATION: /function= "PR-1 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 130..162
, OTHER INFORMATION: /function= "CDR-1 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 163..207
, OTHER INFORMATION: /function= "PR-2 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 208..228
, OTHER INFORMATION: /function= "CDR-2 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 229..324
, OTHER INFORMATION: /function= "PR-3 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 325..351
, OTHER INFORMATION: /function= "CDR-3 sequence"
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, FEATURE:
, NAME/KEY: misc.feature
, LOCATION: 352..381
, OTHER INFORMATION: /function= "PR-4 sequence"
,
, US-08-574-699A-1

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|    | Query Match               | 91.5%; Score 348.6; DB 2; Length 381;                                 |
|    | Best Local Similarity     | 95.0%; Pred. No. 9.5e-102;  |
|    | Matches 360; Conservative | 0; Mismatches 19; Indels 0; Gaps 0;                                   |
| Qy | 1                         | ATGTGTCCTCAGCTCAGTTCCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT 60       |
| Dd | 1                         | ATGTGFHCTTCAGCTCAGTTCCTTGTTCTCTGTTCTCTGTTTTCAAGTTACCATGT 60           |
| Qy | 61                        | GATATCCAGATGCACAGACTACATCTCTCCTGTCCTCTCTCGGAGACAGATCAC 120            |
| Dd | 61                        | GATATCCAGATGCACAGACTACATCTCTCCTGTCGCCCTCTCTCGGAGACAGATCATC 120        |
| Qy | 121                       | ATCAGTTGTCAGGGGAAGTCAGGCATTAGCAGTAATTATAA CTGGTATCACAGAAACCA 180      |
| Dd | 121                       | ATCAGTTGTCAGGGGAAGTCAGGCATTAGCAA TATTTAAGCTGGTATCAACAAGGCCA 180       |
| Qy | 181                       | GATCGAACATATAAACTCCTGATCTACTACACATCAAGATTFACACTCAGGAGTCCCATCA 240     |
| Dd | 181                       | GATCGAAC TGTTAAACTCCTGATCTTCTACACATCAAAA TTACACTCAGGAGTCCCCATCA 240   |
| Qy | 241                       | AGTTCAGTGGCAGTGGGTCTGGAA CAGATTA TTTCTTCACACATTAA CAACCTGGAGCAA 300   |
| Dd | 241                       | AGA TTCAGTGGCAGTGGGTCTGGAA CAGATTA TTTCTTCACACATTAG TAACCTGGACCAA 300 |
| Qy | 301                       | GAACACATTGCCACTTACTTTTGGCAACAGGGTAACGCTTC CGTACACGTTCCGGAGG 360       |
| Dd | 301                       | GAAGATATTGCCACTTACTTTTGGCAACAGGGTAATACGTT TCCTGTAACGTTCCGGAGG 360     |
| Qy | 361                       | GGGACCAAGCTGGAAATAA 379   |
| Dd | 361                       | GGGACAAAGGTGGAAATGA 379   |

RESULT 7  
US-08-137-117D-36  
; Sequence 36, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; \* APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose

```

; TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES:  158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/137,117D
; FILING DATE:  20-DEC-1993
; CLASSIFICATION:  530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  WO PCT/JP92/00544
; FILING DATE:  24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  JP 4-32084
; FILING DATE:  19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  JP 3-95476
; FILING DATE:  25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME:  WEGNER, Harold C.
; REGISTRATION NUMBER:  25,258
; REFERENCE/DOCKET NUMBER:  53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (202)672-5300
; TELEFAX:  (202)672-5399
; TELEX:  904136
; INFORMATION FOR SEQ ID NO:  36:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  381 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  1..381
; FEATURE:
; NAME/KEY:  mat_peptide
; LOCATION:  1..381
; US-08-137-117D-36

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| Query Match           | 90.9%          | Score 346.4        | DB 1     | Length 381   |
|-----------------------|----------------|--------------------|----------|--|
| Best Local Similarity | 94.5%          | Pred. No. 4.8e-101 |          |  |
| Matches 359           | Conservative 0 | Mismatches 21      | Indels 0 | Gaps 0   |
| Qy                    | 1              | ATG                | GTG      | CCCTCAGCTCAGTTCCTTGGTCTCCTCTGCTCTGTTTCAAGGTACCAGATGT 60      |
|                       |                |                    |          |  |
| Db                    | 1              | ATG                | GTG      | TCCACACCTCAGTTCCTTGGTCTCCTGTGTGATCTGTTTCAAGGTACCAGATGT 60    |
|                       |                |                    |          |  |
| Qy                    | 61             | GAT                | ATC      | CAGATGACACAGACTACATCTCCTGTCTCCTCTCTGCGAGACAGAGTCACC 120      |
|                       |                |                    |          |  |
| Db                    | 61             | GAT                | ATC      | CAGATGACACAGACTACATCTCCTGTCTGCTCTCTGGGAGACAGAGTCACC 120      |
|                       |                |                    |          |  |
| Qy                    | 121            | ATC                | AGTTG    | CAGGCGAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180     |
|                       |                |                    |          |  |
| Db                    | 121            | ATC                | AGTTG    | CAGGCGAAGTCAGGACATTTAGTAAATTTTAACTGGTATCAACAGAAACCA 180      |
|                       |                |                    |          |  |
| Qy                    | 181            | GAT                | GGA      | ACTATTTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCCATCA 240   |
|                       |                |                    |          |  |
| Db                    | 181            | GAT                | GGA      | ACTGTTTAAACTCCTGATCTACTATACATCAAGATTACACTCAGGAGTCCCCATCA 240 |
|                       |                |                    |          |  |
| Qy                    | 241            | AGG                | TTC      | AGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAAACCTGGAGCAA 300   |
|                       |                |                    |          |  |
| Db                    | 241            | AGG                | TTC      | AGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAGCAACTGGAGCAA 300  |
|                       |                |                    |          |  |

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Db 301 GAAGATATTGCCAGTTACTTTTCCCAACAGGCTTATACGCTCCGTTGACGTTCCGTTGGA 360  
QY 361 GGGACCAAGCTGGAATAAA 380  
Db 361 GGCACCAAGTTGGAATCAA 380

RESULT 8  
US-08-436-717-36  
; Sequence 36, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..381  
US-08-436-717-36

Query Match 90.9%; Score 346.4; DB 1; Length 381;

Best Local Similarity 94.5%; Pred. No. 4.8e-101;  
Matches 359; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 1 ATGTTGTCCTCAGTCTCAGTTCCCTTGGTCTCTCTGTTCTGTTTCAAGGTACAGATGT 60  
Db 1 ATGTTGTCCTCAGTCTCAGTTCCCTTGGTCTCTCTGTTCTGTTTCAAGGTACAGATGT 60  
QY 61 GATATCCAGATGACACAGACTACATCTCTCCCTGTCCTCTCTGGGAGACAGAGTACCC 120  
Db 61 GATATCCAGATGACACAGACTACATCTCTCCCTGTCCTCTCTGGGAGACAGAGTACCC 120  
QY 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180  
Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGTAAATTTATTTAACTGGTATCAGCAGAAACCA 180  
QY 181 GATGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240  
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QY 241 AGGTTCACTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTCGAGCAA 300  
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QY 301 GAAGACATTCGCACTTACTTTTGCCAAACAGGTTAACACGTTCCGTACACGTTCCGAGGG 360  
Db 301 GAAGATATTGCCAGTTACTTTTGCCAAACAGGTTTATAGCCCTCGTGGAGCTTCGGTGA 360  
QY 361 GGCACCAAGCTGGAATAAA 380  
Db 361 GGCACCAAGTTGGAATCAA 380

RESULT 9  
US-08-836-561-28  
; Sequence 28, Application US/08836561  
; Patent No. 6018032  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masamichi  
; APPLICANT: FURUYA, Akiko  
; APPLICANT: NAKAMURA, Kazuyasu  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: ANAZAWA, Hideharu  
; APPLICANT: HANAI, No. 6018032uo  
; TITLE OF INVENTION: Antibody Against Human Interleukin-5  
; TITLE OF INVENTION: Receptor Alpha Chain  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741



[illegible]





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; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
; NAME/KEY: CDS
; LOCATION: (25)..(408)
; NAME/KEY: mat_peptide
; LOCATION: (85)..(408)
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US-09-225-322B-9

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Best Local Similarity 90.5%; Pred.No.2.e-93;
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0

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QY      25 ATGATGTCCTTCGTCAGTTCCTTTGGTGCTCCTCGTTGCTCTGTTTTCAAGGTACCAGATGT 84
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 GATA TC CAGATGACACAGACTACATCCCTCCTGCCTGCTCTCTGGGAGACAGAGTCACC 120
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QY      85 GATA TC CAGATGACACAGACTGCATCCCTCCCTGCTGCTCTCTCTGGGAGACAGAGTCACC 144
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QY     121 ATCAGTTGCCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTCGTATCACGACAGAACCA 180
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     145 ATCAGTTGCAGTGCAGTCAGGACATTAGTAATTTATTTAAACTGGTATCAACAGAACCA 204
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QY     181 GATGGAACTATTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCACATCA 240
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     205 GATGGAACTGTTAAACTCCTCATCTTTTACTCATCAAATTTACACTCGGGAGTCCCACATCA 264
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     241 AGGTTTCAGTGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     265 AGGTTTCAGTGGCGGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAGCCT 324
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QY     301 GAAGACATTGCACCTTACTTTTTCGCAACAGGGTAACAGCCTTCGCGTACACCGTTGGAGGG 360
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     325 GAAGATATTGCCACTTACTTTTGTTCATCAGTATAGTAGCTTCGTTGGACGCTTCGGTGA 384
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     361 GGGACCAAGCTGGAAATAA 380
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     385 GGCACCAAGCTGGAAATAA 404
Db              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 15  
US-09-764-304-9  
; Sequence 9, Application US/09764304  
; Patent No. 6495666  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUNAWA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764.304  
; CURRENT FILING DATE: 2001-01-19

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; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(408)
; NAME/KEY: mat_peptide
; LOCATION: (85)..(408)
; NAME/KEY: sig_peptide
; LOCATION: (25)..(84)
; US-09-764-304-9

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|-----------------------|--------|--------------|----------|------------|-----|--------|------|------|----|
| Query Match           | 84.5%; | Score        | 322.4;   | DB         | 4;  | Length | 408; |      |    |
| Best Local Similarity | 90.3%; | Pred. No.    | 2.2e-93; |            |     |        |      |      |    |
| Matches               | 344;   | Conservative | 0;       | Mismatches | 36; | Indels | 0;   | Gaps | 0; |

  

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| Qy | 1   | ATGGTGCTCCAGTCAGTTCCTTGGTCTCCTGTGTGCTCTGTGTTTCAAGGTACCAAGATGT | 60  |
| Db | 25  | ATGATGCTCTGCTCAGTTCCTTGGTCTCCTGTGTGCTCTGTGTTTCAAGGTACCAAGATGT | 84  |
| Qy | 61  | GATATCCAGATGACACAGACTACATCCTCTCCTGTCTGTCCTCTCTCGGAGACAGAGTCA  | 120 |
| Db | 85  | GATATCCAGATGACACAGACTGCACTCCTCCTCGCTCTCTCGGAGACAGAGTCA        | 144 |
| Qy | 121 | ATCAGTTGCAGGCCAAGTCAGGACATTTAGCAGATTATTTAAACTGGTATCAGCAGAAA   | 180 |
| Db | 145 | ATCAGTTGCAGTGCAGTCAGGACATTTAGTAAATTTATTTAAACTGGTATCAACAGAA    | 204 |
| Qy | 181 | GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCA     | 240 |
| Db | 205 | GATGGAACTGTTAAACTCCTGATCTTTTACTCATCAAAATTTACACTCGGAGTCCCA     | 264 |
| Qy | 241 | AGGTTTCAGTGGCAGTGGGTCTGAAACAGATTATTCTCTCACCATTACACACCTGG      | 300 |
| Db | 265 | AGGTTTCAGTGGCGGTGGGTCCGGGACAGATTATTTCTCTCACCATTACACACCTGG     | 324 |
| Qy | 301 | GAAGACATTGCCACTTTACTTTTGGCAACAGGGTAAACACGCTTCGGTACACGTTCCG    | 360 |
| Db | 325 | GAAGATATTGCCACTTTACTTTTGTCTCATGATAGTAGTAAGCTTCCGTGGACGTT      | 384 |
| Qy | 361 | GGGACCAAGCTGAAATAAA   | 380 |
| Db | 385 | GGCACCAGCTGGAAATCAA   | 404 |

Search completed: October 24, 2003, 05:50:34  
Job time : 58.8788 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:57:16 ; Search time 904.875 Seconds  
(without alignments)  
1129.179 Million cell updates/sec

Title: US-09-114-285A-28

Perfect score: 381  
Sequence: 1 ATGGTGTCCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
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14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 359.2 | 94.3        | 393    | 8  | US-08-779-784-20   |
| 2          | 359.2 | 94.3        | 393    | 12 | Sequence 20, Appl  |
| 3          | 351.2 | 92.2        | 381    | 12 | Sequence 63, Appl  |
| 4          | 349.6 | 91.8        | 381    | 14 | Sequence 4, Appl   |
| 5          | 338.4 | 88.8        | 382    | 14 | Sequence 1, Appl   |
| 6          | 332.4 | 84.6        | 408    | 9  | Sequence 28, Appl  |
| 7          | 322.4 | 84.6        | 408    | 12 | Sequence 9, Appl   |
| 8          | 322.4 | 84.6        | 408    | 14 | Sequence 9, Appl   |
| 9          | 320.8 | 84.2        | 408    | 14 | Sequence 9, Appl   |
| 10         | 309.6 | 81.3        | 382    | 14 | Sequence 102, Appl |
| 11         | 304.8 | 80.0        | 382    | 14 | Sequence 97, Appl  |
| 12         | 301.6 | 79.2        | 382    | 14 | Sequence 70, Appl  |
| 13         | 301.6 | 79.2        | 382    | 14 | Sequence 91, Appl  |
| 14         | 300   | 78.7        | 382    | 14 | Sequence 87, Appl  |
| 15         | 299.2 | 78.5        | 324    | 8  | Sequence 22, Appl  |
| 16         | 294.4 | 77.3        | 324    | 13 | Sequence 3, Appl   |

|    |       |      |      |    |                    |
|----|-------|------|------|----|--------------------|
| 17 | 291.2 | 76.4 | 321  | 12 | US-10-310-674A-33  |
| 18 | 289.6 | 76.0 | 324  | 9  | Sequence 33, Appl  |
| 19 | 289.6 | 76.0 | 324  | 14 | Sequence 72, Appl  |
| 20 | 288.2 | 75.6 | 916  | 9  | Sequence 6, Appl   |
| 21 | 288.2 | 75.6 | 1527 | 14 | Sequence 29, Appl  |
| 22 | 288   | 75.6 | 1803 | 10 | Sequence 347, Appl |
| 23 | 276   | 72.4 | 285  | 8  | Sequence 2, Appl   |
| 24 | 262.2 | 68.8 | 315  | 14 | Sequence 23, Appl  |
| 25 | 260.8 | 68.5 | 321  | 11 | Sequence 30, Appl  |
| 26 | 256.4 | 67.6 | 324  | 14 | Sequence 9, Appl   |
| 27 | 256.4 | 67.3 | 306  | 14 | Sequence 3, Appl   |
| 28 | 254   | 66.7 | 324  | 14 | Sequence 28, Appl  |
| 29 | 252   | 66.1 | 435  | 9  | Sequence 13, Appl  |
| 30 | 250.4 | 65.7 | 402  | 8  | Sequence 1, Appl   |
| 31 | 250.4 | 65.7 | 402  | 12 | Sequence 5, Appl   |
| 32 | 250.4 | 65.7 | 402  | 12 | Sequence 5, Appl   |
| 33 | 247.2 | 64.9 | 407  | 10 | Sequence 27, Appl  |
| 34 | 245.4 | 64.4 | 307  | 14 | Sequence 9, Appl   |
| 35 | 243   | 63.8 | 708  | 12 | Sequence 3, Appl   |
| 36 | 242.4 | 63.6 | 974  | 10 | Sequence 29, Appl  |
| 37 | 239.2 | 62.8 | 390  | 12 | Sequence 10, Appl  |
| 38 | 239.2 | 62.8 | 714  | 14 | Sequence 18, Appl  |
| 39 | 239.2 | 62.8 | 729  | 12 | Sequence 125, App  |
| 40 | 239.2 | 62.8 | 729  | 14 | Sequence 125, App  |
| 41 | 237.2 | 62.3 | 520  | 10 | Sequence 1210, Ap  |
| 42 | 237.2 | 62.3 | 520  | 13 | Sequence 1210, Ap  |
| 43 | 237.2 | 62.3 | 520  | 14 | Sequence 1210, Ap  |
| 44 | 236   | 61.9 | 387  | 9  | Sequence 1, Appl   |
| 45 | 234.4 | 61.5 | 387  | 9  | Sequence 27, Appl  |

#### ALIGNMENTS

#### RESULT 1

US-08-779-784-20  
; Sequence 20, Application US/08779784  
; Publication No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
; TELECOMMUNICATION INFORMATION:



Db 61 GATATCCAGATGACACAGACTACATCTCCTGTCTCCCTCTCTGGGAGACAGAGTCACC 120  
Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180  
Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180  
Qy 181 GATGGAACATTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 181 GATGGAACATTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Qy 241 AGGTTTCAGTGGCAGTGGTCTGGAAACAGATTATCTCTCACCATTAAACAACCTGGAGCA 300  
Db 241 AGGTTTCAGTGGCAGTGGTCTGGAAACAGATTATCTCTCACCATTAAACAACCTGGAGCA 300  
Qy 301 GAAGACATTGCCACTTACTTTTGCACACAGGTAACAGCTTCCGTACAGCTTCGGAGGG 360  
Db 301 GAAGATATTGCCACTTACTTTTGCACACAGGTAACAGCTTCCGTACAGCTTCGGAGGG 360  
Qy 361 GGGACCAAGCTGGAATAAA 380  
Db 361 GGCACCAAGCTGGAATACAA 380

## RESULT 4

US-10-084-139-1  
; Sequence 1, Application US/10084139  
; Publication No. US20030109416A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: YATOMI, Takehiro  
; APPLICANT: SUDA, Takashi  
; TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT  
; FILE REFERENCE: 1110-0307P  
; CURRENT APPLICATION NUMBER: US/10/084.139  
; CURRENT FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(381)  
US-10-084-139-1

Query Match 91.8%; Score 349.6; DB 14; Length 381;  
Best Local Similarity 95.0%; Pred. No. 2.3e-107;  
Matches 361; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ATGGTGTCTCAGCTCAGTCTCTGGTCTCCTGCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60  
Db 1 ATGATGTCTCTGCTCAGTCTCTGGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60  
Qy 61 GATATCCAGATGACACAGACTACATCTCCTCCTGCTCTCTGGGAGACAGAGTCACC 120  
Db 61 GATATCCAGATGACACAGACTACATCTCCTCCTGCTCTCTGGGAGACAGAGTCACC 120  
Qy 121 ATCAGTTCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180  
Db 121 ATCAGTTCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180  
Qy 181 GATGGAACATTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 181 GATGGAACATTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Qy 241 AGGTTTCAGTGGCAGTGGTCTGGAAACAGATTATTCTCTCACCATTAAACAACCTGGAGCA 300  
Db 241 AGGTTTCAGTGGCAGTGGTCTGGAAACAGATTATTCTCTCACCATTAAACAACCTGGAGCA 300  
Qy 301 GAAGACATTGCCACTTACTTTTGGCAACAGGGTAACAGCTTCCGTACACGTTTCGGAGGG 360  
Db 301 GGAGATATTGCCACTTACTTTTGGCAACAGGGTAGTAGCTTCCGTGGACGTTCCGGTGA 360

Qy 361 GGGACCAAGCTGGAATAAA 380  
Db 361 GGCACCAAGCTGGAATACAA 380

## RESULT 5

US-10-283-349-28  
; Sequence 28, Application US/10283349  
; Publication No. US20030096977A1  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masamichi  
; FURUYA, Akiko  
; NAKAMURA, Kazuyasu  
; IIDA, Akihiro  
; ANAZAWA, Hideharu  
; HANAI, No. US20030096977A1uo  
; TAKATSU, Kiyoshi  
; TITLE OF INVENTION: Antibody Against Human Interleukin-5  
; Receptor Alpha Chain  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/283.349  
; FILING DATE: 29-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836.561  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: JP 232384/95  
; FILING DATE: 11-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lawrence, III, Stanton T  
; REGISTRATION NUMBER: 25,736  
; REFERENCE/DOCKET NUMBER: 7005-115-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 382 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-10-283-349-28

Query Match 88.8%; Score 338.4; DB 14; Length 382;  
Best Local Similarity 93.2%; Pred. No. 1.4e-103;  
Matches 354; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 ATGTGTCTCAGTCTAGTTCCTTGGTCTCTGCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60  
Db 1 ATGATGTCTCTGCTCAGTTCCTTGGTCTCTGCTCTGTTTCAAGGTATCAGATGT 60  
Qy 61 GATATCCAGATGACACAGACTACATCTCCTGCTCTCTGGGAGACAGAGTCACC 120  
Db 61 GATATCCAGATGACACAGGCTACATCTCCTGCTCTCTGGGAGACAGAGTCACC 120  
Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180

Db 121 ATCGGTTGGGACAAAGTGGAGACATTATCAATATTTAACTGGTATCGGAAGAAACCA 180  
QY 181 GATGGAACCTATTAAACTCTGTACTTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 181 GATGGAACCTATTAAACTCTGTACTTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
QY 241 AGGTTTCAGTGGCAGTGGGCTCGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300  
Db 241 AGGTTTCAGTGGCAGTGGGCTCGGAACAGATTATTTCTCACCATTAGTACCTGGAGCAA 300  
QY 301 GAAGACATTGCCACTTACTTTTGGCAACAGGTTAAACAGCTTCCGTACACGTTGGAGGG 360  
Db 301 GAAGATATTGCCACTTACTTTTGGCAACAGGTTTATACGTTCCGTACACGTTGGAGGG 360  
QY 361 GGGACCAAGCTGGAAATAAA 380  
Db 361 GGGACCAAGTGGAAATAAA 380

RESULT 6  
US-09-764-304-9  
; Sequence 9, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(408)  
; NAME/KEY: mat\_peptide  
; LOCATION: (85)..(408)  
; NAME/KEY: sig\_peptide  
; LOCATION: (25)..(84)  
US-09-764-304-9

Query Match 84.6%; Score 322.4; DB 9; Length 408;  
Best Local Similarity 90.5%; Pred. No. 3.5e-98;  
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1 ATGGTGCTCTCAGCTCAGTTCCTCGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60  
Db 25 ATGATGCTCTGCTCAGTTCCTCGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 84  
QY 61 GATATCCAGATGACACAGACTACCTCCCTGCTCTGCTCTCTCTGGAGACAGAGTCCACC 120

Db 85 GATATCCAGATGACACAGACTGATCTCCTCGCTGCTCTCTGGGAGACAGAGTCCACC 144  
QY 121 ATCAGTTGCGGGCAAGTTCAGGACATTAGAGTATTTAAACTGTTATTCACAGAAACCA 180  
Db 145 ATCAGTTGCGGGCAAGTTCAGGACATTAGTAAATTTAACTGTTATTCACAGAAACCA 204  
QY 181 GATGGAACCTATTAAACTCTGTACTTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 205 GATGGAACCTATTAAACTCTGTACTTACATCAAAATTTACACTCGGAGTCCCATCA 264  
QY 241 AGGTTTCAGTGGCAGTGGGCTCGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300  
Db 265 AGGTTTCAGTGGGCTGGGTCGGGACAGATTATTTCTCACCATTACAGCAACCTGGAGCCT 324  
QY 301 GAACACATTCGCCACTTACTTTTGGCAACAGGTTAAACAGCTTCCGTACACGTTGGAGGG 360  
Db 325 GAAGATATTGCCACTTACTTTTGTACATAGTATAGTAACTTCCGTGGAGCTTCGGTGA 384  
QY 361 GGGACCAAGCTGGAAATAAA 380  
Db 385 GGCACCAAGCTGGAAATCAA 404

RESULT 7  
US-10-166-626-9  
; Sequence 9, Application US/10166626  
; Publication No. US20030166876A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/166,626  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/225,322B  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(408)  
; NAME/KEY: mat\_peptide  
; LOCATION: (85)..(408)  
; NAME/KEY: sig\_peptide  
; LOCATION: (25)..(84)  
US-10-166-626-9

Query Match 84.6%; Score 322.4; DB 12; Length 408;  
Best Local Similarity 90.5%; Pred. No. 3.5e-98;  
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1 ATGGTGCTCTCAGCTCAGTTCCTCGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60

Db 25 ATGATGCTCTGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 84  
Qy 61 GATATCCAGATGACACAGACTACATCCTCCCTGCTCTCTGGGAGACAGAGTCAAC 120  
Db 85 GATATCCAGATGACACAGACTGCAATCCTCCCTGCTCTCTGGGAGACAGAGTCAAC 144  
Qy 121 ATCAGTTCGAGGCAAGTACAGACATTAGCAGTATTTAACTGGTATCAGCAGAAACCA 180  
Db 145 ATCAGTTCGAGTCAAGTACAGACATTAGTAAATTTAACTGGTATCAGCAGAAACCA 204  
Qy 181 GATGAACTATTAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 205 GATGAACTGTTAACTCCTGATCTTTTACTCATCAAAATTTACACTCGGAGTCCCATCA 264  
Qy 241 AGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTTAACTCGGAGCA 300  
Db 265 AGTTTCAGTGGGTGGGTCTGGGACAGATTATTTCTCACCATCAGCAACTCGGAGCT 324  
Qy 301 GAAGACATTCGACCTACTTTTGGCAACAGGGTAAACGCTTCCGTACACGTTCCGAGGG 360  
Db 325 GAAGATATTCGACCTACTTTTGTGTCATCAGTATAGTAACTTCCGTGGAGCTTCGGTGA 384  
Qy 361 GGGACCAAGCTGGAATAAA 380  
Db 385 GGCACCAAGCTGGAATACAA 404

## RESULT 8

US-10-265-713-9  
; Sequence 9, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641  
; NAME/KEY: CDS  
; LOCATION: (25)..(408)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (85)..(408)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (25)..(84)  
US-10-265-713-9

Query Match 84.6%; Score 322.4; DB 14; Length 408;  
Best Local Similarity 90.5%; Pred. No. 3.5e-98;  
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
Qy 1 ATGGTGCCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 60  
Db 25 ATGATGCTCTGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACCAGATGT 84  
Qy 61 GATATCCAGATGACACAGACTACATCCTCCCTGCTCTCTGGGAGACAGAGTCAAC 120  
Db 85 GATATCCAGATGACACAGACTGCAATCCTCCCTGCTCTCTGGGAGACAGAGTCAAC 144  
Qy 121 ATCAGTTCGAGGCAAGTACAGACATTAGCAGTATTTAACTGGTATCAGCAGAAACCA 180  
Db 145 ATCAGTTCGAGTCAAGTACAGACATTAGTAAATTTAACTGGTATCAGCAGAAACCA 204  
Qy 181 GATGAACTATTAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
Db 205 GATGAACTGTTAACTCCTGATCTTTTACTCATCAAAATTTACACTCGGAGTCCCATCA 264  
Qy 241 AGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTTAACTCGGAGCA 300  
Db 265 AGTTTCAGTGGGTGGGTCTGGGACAGATTATTTCTCACCATCAGCAACTCGGAGCT 324  
Qy 301 GAAGACATTCGACCTACTTTTGGCAACAGGGTAAACGCTTCCGTACACGTTCCGAGGG 360  
Db 325 GAAGATATTCGACCTACTTTTGTGTCATCAGTATAGTAACTTCCGTGGAGCTTCGGTGA 384  
Qy 361 GGGACCAAGCTGGAATAAA 380  
Db 385 GGCACCAAGCTGGAATACAA 404

## RESULT 9

US-10-195-752-19  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/195,752  
; FILING DATE: 16-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B  
; FILING DATE: 27-JUN-96  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-195-752-19

Query Match 84.2%; Score 320.8; DB 14; Length 408;  
Best Local Similarity 90.3%; Pred. No. 1.2e-97;  
Matches 343; Conservative 0; Mismatches 37; Indels 0; Gaps 0;





RESULT 13  
US-10-283-349-91

[illegible]

RESULT 15  
US-08-779-784-22  
; Sequence 22, Application US/08779784  
; Publication No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:03:25 ; Search time 57.2462 Seconds  
(without alignments)  
352.133 Million cell updates/sec

Title: US-09-114-285a-29

Perfect score: 661

Sequence: 1 MVSSAFLGALLLCFQSTRC.....COQNTLPYTFGGTKLEIN 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 19Jun03:\*

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24: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Query | Score | Match | Length | ID       | Description        |
|------------|-------|-------|-------|--------|----------|--------------------|
| 1          | 661   | 100.0 | 127   | 13     | AAR28670 | pPM-k3 protein pro |
| 2          | 638   | 96.5  | 131   | 16     | AAR84553 | MAB SCH94.03 light |
| 3          | 627   | 94.9  | 127   | 14     | AAR32121 | Anti-CD4 antibody  |
| 4          | 621   | 93.9  | 127   | 18     | AAW11815 | Mouse anti-human F |
| 5          | 621   | 93.9  | 127   | 19     | AAW60033 | Mouse antibody F91 |
| 6          | 621   | 93.9  | 128   | 11     | AAR09426 | ME4 Light Chain V  |
| 7          | 621   | 93.9  | 128   | 18     | AAW06215 | MAB ME4 light chai |
| 8          | 621   | 93.9  | 128   | 20     | AAW85062 | Mouse ME4 light ch |
| 9          | 621   | 93.9  | 128   | 24     | ABUS8896 | Mouse antibody lig |

|    |     |      |     |    |          |                     |
|----|-----|------|-----|----|----------|---------------------|
| 10 | 619 | 93.6 | 127 | 14 | AAR39265 | Mouse C4G1 Ig light |
| 11 | 619 | 93.6 | 127 | 17 | AAW49809 | Variable region of  |
| 12 | 606 | 91.7 | 127 | 17 | AAR99003 | MAB VL17E6 light c  |
| 13 | 599 | 90.6 | 127 | 13 | AAR29010 | p146-k3 protein pr  |
| 14 | 590 | 89.3 | 126 | 12 | AAR12237 | Mouse MAB 1C11 L c  |
| 15 | 590 | 89.3 | 127 | 12 | AAR12359 | Light (kappa) chai  |
| 16 | 587 | 88.8 | 124 | 15 | AAR47206 | Human/murine IL-1   |
| 17 | 574 | 86.8 | 128 | 21 | AAW01628 | Murine immunoglob   |
| 18 | 574 | 86.8 | 128 | 22 | AAW81978 | Ganglioside GD3 sp  |
| 19 | 574 | 86.8 | 128 | 24 | ABU11003 | Modified ganglios   |
| 20 | 573 | 86.7 | 128 | 14 | AAR33257 | Rat immunoglobulin  |
| 21 | 566 | 85.6 | 128 | 20 | AAW28368 | pK641 LA2 immunog   |
| 22 | 559 | 84.6 | 128 | 15 | AAW53340 | KM641 H chain vari  |
| 23 | 556 | 84.1 | 127 | 18 | AAW21844 | Light chain variab  |
| 24 | 537 | 81.2 | 634 | 24 | ABW22300 | CD19:zeta chimeric  |
| 25 | 534 | 80.8 | 107 | 24 | ABJ18571 | Ganglioside-associ  |
| 26 | 534 | 80.8 | 107 | 24 | ABJ18574 | Ganglioside-associ  |
| 27 | 534 | 80.8 | 108 | 21 | AAW94216 | Murine consensus 1  |
| 28 | 533 | 80.6 | 128 | 22 | AAW81999 | Ganglioside GD3 sp  |
| 29 | 526 | 79.6 | 107 | 19 | AAW66098 | anti-CD22 monoclon  |
| 30 | 526 | 79.6 | 128 | 22 | AAW81994 | Ganglioside GD3 sp  |
| 31 | 526 | 79.6 | 233 | 22 | AAW49242 | Chimeric 4H6 anti-  |
| 32 | 525 | 79.4 | 128 | 22 | AAW81995 | Ganglioside GD3 sp  |
| 33 | 525 | 79.4 | 895 | 23 | AAW75368 | Diphtheria toxin/U  |
| 34 | 525 | 79.4 | 895 | 23 | AAU75369 | Diphtheria toxin/U  |
| 35 | 525 | 79.4 | 895 | 23 | AAU75374 | Diphtheria toxin/U  |
| 36 | 525 | 79.4 | 896 | 23 | AAU75366 | Diphtheria toxin/U  |
| 37 | 525 | 79.4 | 896 | 23 | AAU75367 | Diphtheria toxin/U  |
| 38 | 525 | 79.4 | 896 | 23 | AAU75373 | Diphtheria toxin/U  |
| 39 | 525 | 79.4 | 899 | 23 | AAU75375 | Diphtheria toxin/U  |
| 40 | 524 | 79.3 | 107 | 14 | AAR30768 | Murine anti-CD3 MA  |
| 41 | 524 | 79.3 | 601 | 21 | AAW07461 | An immunotoxin com  |
| 42 | 524 | 79.3 | 601 | 24 | ABG72265 | Recombinant immuno  |
| 43 | 524 | 79.3 | 637 | 23 | AAU75365 | Diphtheria toxin/U  |
| 44 | 524 | 79.3 | 638 | 23 | AAU75370 | Diphtheria toxin/U  |
| 45 | 524 | 79.3 | 642 | 23 | AAU75382 | Diphtheria toxin/U  |

#### ALIGNMENTS

#### RESULT 1

AAW28670.

ID AAR28670 standard; Protein; 127 AA.

XX AC AAR28670;

XX DT 25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

XX DE pPM-k3 protein product.

XX KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;

KW heavy chain; variable region; mouse; monoclonal; hybridoma; PMI;

XX plasmid; pPM-k3; pPM-h1.

XX OS Synthetic.

XX FH Key

FT Peptide

FT Protein

FT FT

XX WO9219759-A1.

XX PD 12-NOV-1992.

XX PF 24-APR-1992;

XX PR 25-APR-1991;

XX PR 19-FEB-1992;

XX

Location/Qualifiers  
1..20  
/note= "Signal peptide"  
21..127  
/note= "Mature peptide"

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```

PA (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
PI
XX WPI; 1992-398882/48.
DR N-PSDB; AAQ30755.
XX
XX Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PT
XX
XX Disclosure; Page 121-122; 207pp; Japanese.
XX
XX The sequences given in AAR28670-71 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 127 AA;
SQ
Query Match 100.0%; Score 681; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3e-43;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
DB 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
QY 121 GTKLEIN 127
DB 121 GTKLEIN 127
RESULT 2
AAR84553
ID AAR84553 standard; Protein; 131 AA.
XX
XX AAR84553;
XX
XX 02-FEB-1996 (first entry)
XX
XX MAB SCH94.03 light chain.
XX
XX Monoclonal antibody; MAB; SCH94.03; hybridoma; central nervous system;
KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /label= Leader_peptide
FT Region 44..54
FT /label= CDR1
FT Region 70..76
FT /label= CDR2
FT Region 109..117
FT /label= CDR3
FT Region 116..128
FT /label= Joining_region
FT Region 129..131
FT /label= C-kappa_region
XX
XX WO9530004-A1.
PN
XX
XX 09-NOV-1995.
XX
XX

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PF 27-APR-1995; 95WO-USO5262.
XX
XX 29-APR-1994; 94US-0236520.
XX
XX (MAYO-) MAYO FOUNDATION.
XX
XX Miller DJ, Rodriguez M;
PI
XX WPI; 1995-393077/50.
DR N-PSDB; AAR05311.
XX
XX Monoclonal antibodies which stimulate central nervous system
PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT treating multiple sclerosis, and viral or post-neural diseases of
PT the CNS.
XX
XX Disclosure; Page 36-37; 63pp; English.
XX
XX Hybridoma ATCC CRL 11627 was obt'd. from a SJL/J mouse injected with
CC spinal cord homogenate from a mammal uninfected with any
CC demyelinating disease. The hybridoma produced a monoclonal antibody
CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC light chain amino acid sequence is given in AAR84553.
XX
XX Sequence 131 AA;
SQ
Query Match 96.5%; Score 638; DB 16; Length 131;
Best Local Similarity 96.0%; Pred. No. 7.8e-42;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
DB 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
QY 121 GTKLEI 126
DB 121 GTKLEI 126
RESULT 3
AAR32121
ID AAR32121 standard; Protein; 127 AA.
XX
XX AAR32121;
XX
XX 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 02-JUN-1993 (first entry)
XX
XX Anti-CD4 antibody MT 15.1 light chain variable region.
XX
XX immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAB;
KW interleukin-2 receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /label= signal
FT Region 21..115
FT /label= Variable
FT Region 116..127
FT /label= J2
XX
XX DE4143214-A1.
PN
XX
XX 28-JAN-1993.
XX
XX

```

PF 30-DEC-1991; 91DE-4143214.  
 XX 25-JUL-1991; 91DE-4124759.  
 PR 30-DEC-1991; 91DE-4143214.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Kaluza B, Riethmueller G, Scheuer W, Weidle U;  
 XX  
 DR WPI; 1993-037582/05.  
 DR N-PSDB; AAQ36607.  
 XX  
 XX Synergistic antibody compsn. for use as immunosuppressant -  
 FT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 FT alpha- or anti-IL2R beta antibodies  
 XX  
 PS Claim 5; Page 9; 18pp; German.  
 XX  
 CC This sequence is the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAB MT 15.1 is deposited as clone 15-1/P3/14 (ECACC  
 CC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together their immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See also AAQ36608-036616.  
 CC (Updated on 10-MAR-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 127 AA;  
 Query Match 94.9%; Score 627; DB 14; Length 127;  
 Best Local Similarity 93.7%; Pred. No. 5.3e-41;  
 Matches 118; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 Db 1 MMSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDINNLSWYQOKP 60  
 Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPYTFGG 120  
 Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPYTFGG 120  
 Qy 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 4  
 AAW11815  
 ID AAW11815 standard; Protein; 127 AA.  
 XX  
 AC AAW11815;  
 XX  
 DT 20-OCT-1997 (first entry)  
 XX  
 DE Mouse anti-human Fas ligand antibody F919 light chain.  
 XX  
 KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;  
 KW induction; assay; enzyme linked immunosorbant assay; diagnosis;  
 KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;  
 KW graft versus host disease; ulcerative colitis; sequelae;  
 KW myocardial infarction; mouse; murine; monoclonal; treatment;  
 KW complementarity determining region; CDR.  
 XX  
 OS Mus spp.  
 XX  
 XX Key Location/Qualifiers  
 FH 44..54  
 FT Region. /label= CDR\_1  
 FT 70..76  
 FT Region

FT /label= CDR\_2  
 FT 109..117  
 FT /label= CDR\_3  
 XX  
 PN WO9702290-A1.  
 XX  
 PD 23-JAN-1997.  
 XX  
 XX 01-JUL-1996; 96WO-JP01820.  
 XX  
 XX 17-MAY-1996; 96US-0649100.  
 PR 30-JUN-1995; 95JP-0188480.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 PI Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;  
 XX  
 DR WPI; 1997-108917/10.  
 DR N-PSDB; AAT59500.  
 XX  
 PT Antibody reactive with Fas ligand capable of inducing apoptosis -  
 PT used for diagnostic assay of Fas ligand in body fluids and for  
 PT treatment of diseases in which Fas ligand/Fas antigen is involved  
 XX  
 PS Claim 5; Fig 10; 164pp; Japanese.  
 XX  
 CC The present sequence is the light chain of the mouse  
 CC anti-apoptosis inducing human Fas ligand, monoclonal antibody,  
 CC F919. The antibody can be used in a Fas ligand assay, e.g. an  
 CC enzyme linked immunosorbant assay, to diagnose diseases in which  
 CC the Fas ligand/Fas antigen system is implicated, e.g. hepatitis  
 CC B/C, human immunodeficiency virus, graft/host disorders,  
 CC ulcerative colitis or sequelae of myocardial infarction. The  
 CC antibody may also be used to treat such diseases.  
 XX  
 SQ Sequence 127 AA;  
 Query Match 93.9%; Score 621; DB 18; Length 127;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 Db 1 MMSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPYTFGG 120  
 Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPYTFGG 120  
 Qy 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 5  
 AAW60033  
 ID AAW60033 standard; Protein; 127 AA.  
 XX  
 AC AAW60033;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE Mouse antibody F919-9-18 light chain sequence.  
 XX  
 KW Fas ligand; Fas antagonist; apoptosis related disease; liver disease;  
 KW heart failure; kidney failure; graft-versus-host disease; antibody;  
 KW myocardial infarction; ischemic restenosis; endotoxic shock.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 44..54  
 FT Region 44..54  
 FT

FT Region /note= "complementarity determining region (CDR) 1"  
 FT 70..76  
 FT Region /note= "complementarity determining region (CDR) 2"  
 FT 109..117  
 FT /note= "complementarity determining region (CDR) 3"  
 XX  
 PN WO9818487-A1.  
 XX  
 PD 07-MAY-1998.  
 XX  
 XX 31-OCT-1997; 97WO-JP03978.  
 XX  
 XX 26-SEP-1997; 97JP-0262521.  
 PR 31-OCT-1996; 96JP-0290459.  
 PR 27-DEC-1996; 96JP-0351718.  
 XX  
 XX (MOCH) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 PI Nagata S, Suda T, Yatomi T;  
 XX  
 XX WPI; 1998-271925/24.  
 DR N-PSDB; AAV34426.  
 XX  
 XX Use of Fas antagonist for treatment and prevention of  
 PT apoptosis-related diseases - such as heart or kidney failure,  
 PT graft-versus-host disease or liver disease  
 XX  
 XX Disclosure; Fig 1; 86pp; Japanese.  
 PS  
 XX This represents the light chain of the mouse antibody F919-9-18. This  
 CC is used for generating a mouse anti-human Fas ligand monoclonal antibody.  
 CC The invention provides the use of Fas antagonist as an agent for the  
 CC treatment and prevention of apoptosis-related diseases. The Fas  
 CC antagonist can be a partial Fas antigen peptide containing the  
 CC extracellular part of the protein, but lacking the signal sequence, an  
 CC anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is  
 CC preferably a humanised antibody. The Fas antagonist is used in the  
 CC treatment and prevention of diseases such as myocardial infarction, heart  
 CC failure, ischemic heart disease, acute kidney failure, graft-versus-host  
 CC disease, ischemic restenosis of the heart, liver or kidney, and  
 CC endotoxic shock, and also as an organ preservative in transplantation.  
 CC The agent is of low toxicity but effectively inhibits the Fas/Fas ligand  
 CC system.  
 XX  
 SQ Sequence 127 AA;  
 Query Match 93.9%; Score 621; DB 19; Length 127;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 QY 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYCQCGNTLPYTFGG 120  
 Db 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYCQCGNTLPYTFGG 120  
 QY 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 6  
 AAR09426  
 ID AAR09426 standard; Protein; 128 AA.  
 XX  
 AC AAR09426;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 04-MAR-1993 (first entry)  
 XX

DE ME4 Light Chain V Region (mouse).  
 XX  
 KW Monoclonal antibody; chimera; light; heavy; chain; constant;  
 KW variable; antigen; diagnosis; cancer; tumour.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9002569-A.  
 XX  
 XX 22-MAR-1990.  
 PD  
 XX 06-SEP-1989; 89WO-US03852.  
 XX  
 XX 06-SEP-1988; 88US-0240624.  
 PR 08-SEP-1988; 88US-0241744.  
 PR 13-SEP-1988; 88US-0243739.  
 PR 04-OCT-1988; 88US-0253002.  
 PR 19-JUN-1989; 89US-0367641.  
 PR 21-JUL-1989; 89US-0382768.  
 XX  
 XX (ITGE-) INT GENETIC ENG INC.  
 PA (INGE-) INGENE INT GENETIC.  
 XX  
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;  
 XX  
 XX WPI; 1990-115825/15.  
 DR N-PSDB; AAO08608.  
 XX  
 XX Chimeric mouse-human antibodies - prepd. using genes coding for  
 PT constant human region murine variable region, esp. to 3 tumour  
 PT antigen  
 XX  
 XX Claim 13; Page 123 + Fig 29; 173pp; English.  
 PS  
 XX The sequence is used in the prodn. of a chimeric antibody mol.  
 CC comprising two light chains and two heavy chains, each having a  
 CC constant region (human) and a variable region (murine) having a  
 CC specificity to an antigen bound by murine monoclonal antibody  
 CC (Mab) ME4. The chimeric antibodies can be used for any purpose for  
 CC which the original murine MAb can be used, with the advantage that  
 CC they are more compatible with the human body. They are esp. used for  
 CC the diagnosis and treatment of cancer.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 128 AA;  
 Query Match 93.9%; Score 621; DB 11; Length 128;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
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 Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60  
 QY 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYCQCGNTLPYTFGG 120  
 Db 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYCQCGNTLPYTFGG 120  
 QY 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 7  
 AAW06215  
 ID AAW06215 standard; Protein; 128 AA.  
 XX  
 AC AAW06215;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 13-FEB-1997 (first entry)  
 XX  
 DE Mab ME4 light chain variable region.



XX Chimeric antibody; monoclonal antibody; ME4; antibody engineering;  
 KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;  
 KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.  
 XX Mus sp.  
 XX US5576184-A.  
 XX 19-NOV-1996.  
 XX 27-DEC-1994; 94US-0364001.  
 XX 06-MAY-1991; 91US-0659401.  
 XX 06-SEP-1988; 88US-0240624.  
 XX 08-SEP-1988; 88US-0241744.  
 XX 13-SEP-1988; 88US-0243739.  
 XX 04-OCT-1988; 88US-0253002.  
 XX 19-JUN-1989; 89US-0367641.  
 XX 21-JUL-1989; 89US-0382768.  
 XX 27-DEC-1994; 94US-0364001.  
 XX (XOMA ) XOMA CORP.  
 XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;  
 XX WPI; 1997-011249/01.  
 XX N-PSDB; AAT43440.  
 XX Chimeric mouse-human antibodies - recognise a human tumour antigen,  
 PT used for the treatment and diagnosis of human cancers  
 XX Example 3; Fig 29; 102pp; English.  
 XX The light chain variable region (AAW06215) of mouse monoclonal  
 CC antibody ME4 is the product of a cDNA clone (AAT43440) isolated  
 CC from a ME4 hybridoma cDNA library. MAB ME4 (IgG1) binds to an  
 CC antigen that is expressed on the surface of human lung, breast,  
 CC colon and ovary carcinomas and melanomas, but not on most normal  
 CC adult tissues. The light chain and heavy chain variable regions  
 CC (see also AAW06216) of ME4 can be linked to human constant regions  
 CC and expressed in transformed host cells. Novel mouse-human  
 CC chimeric antibodies (see also AAW06209-14 and AAW06217-18) can be  
 CC produced that have specificity to human tumour antigens for use in  
 CC the treatment and diagnosis of human cancer.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 128 AA;  
 Query Match 93.9%; Score 621; DB 18; Length 128;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDISSYLNWYQOKP 60  
 Db 1 MMSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDIITLYLNWYQOKP 60  
 Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120  
 Db 61 DGTVKLLIYVTSRLHSGVPSRFSGSGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120  
 Qy 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 8  
 AAW85062  
 ID AAW85062 standard; Protein; 128 AA.  
 XX AAW85062;  
 AC AAW85062;  
 XX 20-MAR-2003 (updated)

DT 16-APR-1999 (first entry)  
 XX Mouse ME4 light chain variable region.  
 DE Light chain variable region; murine antibody ME4; antibody ING-1;  
 KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;  
 KW treatment; human cancer.  
 XX Mus sp.  
 XX US5843685-A.  
 XX 01-DEC-1998.  
 XX 06-JUN-1995; 95US-0466034.  
 XX 06-SEP-1989; 89WO-US03852.  
 XX 06-MAY-1991; 91US-0659401.  
 XX 27-DEC-1994; 94US-0364001.  
 XX 06-SEP-1988; 88US-0240624.  
 XX 08-SEP-1988; 88US-0241744.  
 XX 13-SEP-1988; 88US-0243739.  
 XX 04-OCT-1988; 88US-0253002.  
 XX 19-JUN-1989; 89US-0367641.  
 XX 21-JUL-1989; 89US-0382768.  
 XX (XOMA ) XOMA CORP.  
 XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;  
 XX WPI; 1999-044574/04.  
 XX N-PSDB; AAV71158.  
 XX Chimeric antibody specific for human tumour antigen - useful as  
 PT immunoassay, imaging or antitumour agent  
 XX Example 3; Fig 29; 92pp; English.  
 XX The present sequence represents the light chain variable region of  
 CC murine antibody ME4. The sequence was used to create chimeric  
 CC mouse-human immunoglobulins which recognise the human tumour  
 CC antigen bound by antibody ING-1 (produced by hybridoma cell line  
 CC ATCC HB 9812). The chimeric antibodies also have an antigen-binding  
 CC site that competitively inhibits the binding of antibody ING-1, and  
 CC mediate complement-dependent cytotoxicity of target cells or  
 CC antibody-dependent cellular cytotoxicity to target cells. The  
 CC chimeric antibodies can be used for therapeutic purposes in the  
 CC treatment of human cancer.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX SQ Sequence 128 AA;  
 Query Match 93.9%; Score 621; DB 20; Length 128;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDISSYLNWYQOKP 60  
 Db 1 MMSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDIITLYLNWYQOKP 60  
 Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120  
 Db 61 DGTVKLLIYVTSRLHSGVPSRFSGSGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120  
 Qy 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 9  
 ABUS8896  
 ID ABUS8896 standard; Protein; 128 AA.  
 XX

AC ABUS58896;  
 XX DT 16-APR-2003 (first entry)  
 XX DE Mouse antibody light chain variable region #4.  
 XX DE Mouse; human tumour antigen; anti-human tumour antigen-antibody;  
 KW ING-1 antibody; cell line HB9812; immunoassay; imaging;  
 KW tumour diagnosis; tumour therapy; cytostatic;  
 KW light chain variable region.  
 XX OS Mus sp.  
 XX US6461824-B1.  
 XX PN 08-OCT-2002.  
 XX PD  
 XX PF 06-JUN-1995; 95US-0467142.  
 XX PR 06-SEP-1989; 89US-0659401.  
 PR 06-SEP-1989; 89WO-US03852.  
 PR 27-DEC-1994; 94US-0364001.  
 PR 06-SEP-1988; 88US-0240624.  
 PR 08-SEP-1988; 88US-0241744.  
 PR 13-SEP-1988; 88US-0243739.  
 PR 04-OCT-1988; 88US-0253002.  
 PR 19-JUN-1989; 89US-0367641.  
 PR 21-JUL-1989; 89US-0382768.  
 XX (XOMA ) XOMA TECHNOLOGY LTD.  
 XX PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;  
 XX DR WPI; 2003-196707/19.  
 DR N-PSDB; ABK79238.  
 XX DT Antibody for detecting antigen in animal or killing cells carrying  
 PT antigen comprises human constant region and variable region having  
 PT specificity for human tumor antigen bound by ING-1 antibody -  
 XX Example 3; Fig 29; 101pp; English.  
 XX The invention describes an antibody comprising a human constant region  
 CC and a variable region having specificity for the human tumour antigen  
 CC bound by the ING-1 antibody, where the ING-1 is produced by cell line  
 CC HB9812 as deposited with ATCC, and the antibody has the same affinity as  
 CC the ING-1 for the human tumour antigen. The antibody is useful in an  
 CC immunoassay method for detecting an antigen in a sample by contacting a  
 CC label-detectable antigen in the sample with the antibody, detecting the  
 CC label and relating the detected label to the presence of the antigen; for  
 CC use in an imaging method for revealing the presence of a label-detectable  
 CC antigen in an animal by contacting the antibody with a part of the animal  
 CC suspected of containing the antigen, detecting the label and relating the  
 CC detected label to the presence of the antigen; and for killing cells  
 CC carrying an antigen by contacting the cells with the antibody and  
 CC allowing the killing to occur. The antibodies are useful in tumour  
 CC diagnosis and therapy. The chimeric antibodies bind to the surface of  
 CC human tumour cells but do not bind detectably to normal cells, e.g.,  
 CC fibroblasts, endothelial cells or epithelial cells in the major organs.  
 CC The high biological activity of the chimeric antibodies against human  
 CC tumour cell lines combined with minimal reactivity with normal tissues  
 CC imply that these antibodies may mediate selective destruction of  
 CC malignant tissue. The presence of human rather than murine antigenic  
 CC determinants on the chimeric antibodies increases their resistance to  
 CC rapid clearance from the body relative to the original murine mAbs. This  
 CC resistance to clearance enhances the potential utility of these chimeric  
 CC antibodies, as well as their derivatives, in tumour diagnosis and  
 CC therapy. This is the amino acid sequence of a mouse antibody light chain  
 CC variable region used in the creation of an anti-human tumour  
 CC antigen-antibody.  
 XX Sequence 128 AA;  
 SQ

Query Match 93.9%; Score 621; DB 24; Length 128;  
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;  
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MVSSAQFLGLLLLCFQGTTRCDIQMTQTSSLSASLSDRVITISCRASQDITTYLNWYQOKP 60  
 Db 1 MVSSAQFLGLLLLCFQGTTRCDIQMTQTSSLSASLSDRVITISCRASQDITTYLNWYQOKP 60  
 QY 61 DGTIKLIYYTSRLHSGVPSRFGSGSGTDYSLTNNLEQEDIATYFCQGNLTLPYTFGG 120  
 Db 61 DGTIKLIYYTSRLHSGVPSRFGSGSGTDYSLTNNLEQEDIATYFCQGNLTLPYTFGG 120  
 QY 121 GTKLEI 126  
 Db 121 GTKLEI 126  
 RESULT 10  
 AAR39265  
 ID AAR39265 standard; Protein; 127 AA.  
 XX AC AAR39265;  
 XX DT 25-MAR-2003 (updated)  
 DT 29-NOV-1993 (first entry)  
 XX Mouse C4G1 Ig light-chain.  
 DE Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIb/IIIb;  
 KW monoclonal antibody; platelet agglutination; humanised antibody.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..21 /label= signal\_peptide  
 FT Protein 22..127 /label= light\_chain  
 FT Region 44..54 /label= complementarity\_determining\_region\_1  
 FT Region 70..76 /label= CDR\_2  
 FT Region 109..117 /label= CDR\_3  
 FT WO9313133-A1.  
 XX 08-JUL-1993.  
 XX 15-DEC-1992; 92WO-JP01630.  
 XX 20-DEC-1991; 91US-0812111.  
 PR 09-JUN-1992; 92US-0895952.  
 PR 11-SEP-1992; 92US-0944159.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX Co MS, Tso JY;  
 XX WPI; 1993-227275/28.  
 DR N-PSDB; AAQ45662.  
 XX Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA  
 PT protein - for treating disorders related to vascular thrombosis  
 XX Disclosure; Fig 2A; 54pp; Japanese.  
 XX This is the sequence of the mouse C4G1 immunoglobulin light  
 CC chain. See AAR39266 for the heavy chain sequence. The antibody is  
 CC specific for the GPIIb/IIIb protein and inhibits platelet  
 CC agglutination. The Ig is thus useful in the treatment of  
 CC thrombosis.

CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 127 AA;

Query Match 93.6%; Score 619; DB 14; Length 127;  
 Best Local Similarity 92.9%; Pred. No. 2.2e-40;  
 Matches 117; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MVSSAQFLGLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60  
 Db 1 MMSSAQFLGLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDINNLYLNWYQOKP 60  
 Qy 61 DGTIKLIYYTSLRHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120  
 Db 61 DGIVKLLIYYTSLRHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120

Qy 121 GTKLEI 126  
 |||||

Db 121 GTKLEI 126  
 |||||

RESULT 11

AAW49809  
 ID AAW49809 standard; Protein; 127 AA.

AC AAW49809;

DT 25-MAR-2003 (updated)

DT 24-SEP-1998 (first entry)

XX Variable region of mouse antibody C4G1 light chain.

DE Mouse; antibody C4G1; light chain; humanised; immunoglobulin; Ig;  
 KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;  
 KW cancer; acute myocardial infarction; unstable angina; stroke;  
 KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;  
 KW extracorporeal cardiopulmonary circulation.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein 21..127

FT /note= "mature protein"

FT Domain 44..54

FT /note= "complementarity determining region"

FT Domain 70..76

FT /note= "complementarity determining region"

FT Domain 109..117

FT /note= "complementarity determining region"

XX US5777085-A.

PN

XX 07-JUL-1998.

XX 17-MAY-1995; 95US-0458516.

XX 03-MAY-1993; 93US-0059159.

XX 20-DEC-1991; 91US-0812111.

XX 09-JUN-1992; 92US-0895952.

XX 11-SEP-1992; 92US-0944159.

XX (PROT-) PROTEIN DESIGN LABS INC.

PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX Co MS, Tso JY;

XX WPI; 1998-398136/34.

XX N-PSDB; AAV36741.

XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from  
 PT mouse C4G1 antibody, used for inhibiting platelet aggregation for  
 PT treating cardiovascular and thromboembolic disorders.

XX Disclosure; Fig 2A; 35pp; English.

XX This is the amino acid sequence of the mouse antibody C4G1 light  
 CC chain, used in the method of the invention involving the creation  
 CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.  
 CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting  
 CC platelet aggregation and also the releasing reaction of platelets. The  
 CC Ig can be used for treating cardiovascular diseases and thromboembolic  
 CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,  
 CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,  
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in  
 CC diagnosing the presence and location of a thrombus, or certain types of  
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the  
 CC detection of GPIIb/IIIa antigens or for isolating platelets.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 127 AA;

Query Match 93.6%; Score 619; DB 19; Length 127;

Best Local Similarity 92.9%; Pred. No. 2.2e-40;

Matches 117; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60

Db 1 MMSSAQFLGLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDINNLYLNWYQOKP 60

Qy 61 DGTIKLIYYTSLRHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120

Db 61 DGIVKLLIYYTSLRHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120

Qy 121 GTKLEI 126  
 |||||

Db 121 GTKLEI 126  
 |||||

RESULT 12

AAW99003

ID AAW99003 standard; Protein; 127 AA.

AC AAW99003;

XX 10-JAN-1997 (first entry)

XX Mab VL1756 light chain (specific for human alphav integrins).

XX Monoclonal antibody; Mab; integrin; cell-matrix interaction;  
 KW tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;  
 KW imaging; detection; radiolabel.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 21..43

FT /label= Framework region 1

FT Binding-site 44..54

FT /label= CDR1

FT Region 55..69

FT /label= Framework region 2

FT Binding-site 70..76

FT /label= CDR2

FT Region 77..108

FT /label= Framework region 3

FT Binding-site 109..117

FT /label= CDR3

FT Region 118..127

FT /label= Framework region 4

XX EP719859-A1.

XX 03-JUL-1996.

XX 06-DEC-1995; 95EP-0119233.

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XX PR 20-DEC-1994; 94EP-0120165.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;
XX PI Rosell E;
XX DR WPI: 1996-302345/31.
XX DR N-PSDB; AAT35050.
XX PT New human integrin V chain-specific monoclonal antibody - and
XX PT related DNA and hybridomas, for treatment and diagnostic imaging of
XX PT tumours, esp melanoma.
XX PS Claim 8; Figure 17a; 54pp; English.
XX CC A monoclonal antibody which reacts only with the alphav chain of
XX CC human alphav integrins; which blocks attachment of alphav integrin
XX CC bearing cells to integrin substrate; which reverses established cell
XX CC matrix interactions caused by alphav integrin; which blocks tumour
XX CC development and which has no cytotoxic activity; may be used to
XX CC treat tumours, especially melanoma (but also glioma, carcinoma)
XX CC optionally coupled to a cytokine such as interleukin-2. The
XX CC monoclonal antibody may also be used for diagnostic imaging of
XX CC tumours and assesment of tumour growth when conjugated to a
XX CC radiolabel or a radio opaque-agent.
XX SQ Sequence 127 AA;
Query Match 91.7%; Score 606; DB 17; Length 127;
Best Local Similarity 90.5%; Pred. No. 2.2e-39;
Matches 114; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISNYLWYQKP 60
Db 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISNYLWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDDIATYFCOQGNTPYTFGG 120
Db 61 DGTVKLLIFYTSKLHSGVPSRFGSGGTDYSLTINNLEQEDDIATYFCOQGNTPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKVEM 126
RESULT 13
AAR29010
ID AAR29010 standard; Protein; 127 AA.
XX AC AAR29010;
XX DT 25-MAR-2003 (updated)
XX DT 30-MAR-1993 (first entry)
XX DE p146-k3 protein product.
XX KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
XX KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
XX KW plasmid; p146-k3; p146-h1.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT /note= "Signal peptide"
XX FT Protein 21..127
XX FT /note= "Mature peptide"
XX PN WO9219759-A1.
XX PD 12-NOV-1992.

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XX PF 24-APR-1992; 92WO-JP00544.
XX PR 25-APR-1991; 91JP-0095476.
XX PR 19-FEB-1992; 92JP-0032084.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX PI WPI; 1992-398882/48.
XX DR N-PSDB; AAQ30759.
XX PT Reconstituted human antibody to human interleukin-6 receptor -
XX PT has low antigenicity and contains mouse V-region complementarity
XX PT determining regions
XX PS Disclosure; Page 127-128; 207pp; Japanese.
XX CC The sequences given in AAR29010-11 were encoded by plasmids which were
XX CC used in example to illustrate the production of a human antibody which
XX CC recognises human interleukin-6 receptor (IL-6R). The antibody which
XX CC comprises light (L) chain and heavy (H) chain variable regions which
XX CC were derived from a mouse monoclonal antibody produced from the
XX CC hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 127 AA;
Query Match 90.6%; Score 599; DB 13; Length 127;
Best Local Similarity 90.5%; Pred. No. 7.5e-39;
Matches 114; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISNYLWYQKP 60
Db 1 MVSTPQFLGLLVICFQGTCDIQMTTSSLSASLGDRVTISCRASQDISNYLWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDDIATYFCOQGNTPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDDIATYFCOQGNTPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKLEI 126
RESULT 14
AAR12237
ID AAR12237 standard; Protein; 126 AA.
XX AC AAR12237;
XX DT 25-MAR-2003 (updated)
XX DT 19-AUG-1991 (first entry)
XX DE Mouse Mab 1C11 L chain, V region.
XX KW HIV-1; chimera.
XX OS Mus sp.
XX PN WO9107494-A.
XX PD 30-MAY-1991.
XX PF 13-NOV-1990; 90WO-US06627.
XX PR 13-NOV-1989; 89US-0433703.
XX PA (XOMA ) XOMA CORP.
XX PA (GREC ) GREEN CROSS CORP.
XX PA (ZOMA-) ZOMA CORP.

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PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX WPI; 1991-178106/24.
DR N-PSDB; AAQ12017.
XX New chimeric mouse human antibodies - used in treatment, diagnosis
PT and prophylaxis of HIV infections.
XX Disclosure; Fig 13; 108pp; English.
XX The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 126 AA;
Query Match 89.3%; Score 590; DB 12; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.7e-38;
Matches 113; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Qy 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
Search completed: October 22, 2003, 22:16:35
Job time : 59.2462 secs

CC This is the light (kappa)- chain variable (V) region of a mouse
CC monoclonal antibody (MAB), 1C11, and is specific for an HIV-1
CC viral antigen. It is used in the construction of a chimeric
CC MAB comprising heavy and light chains having murine V regions
CC and human C regions. The chimeric MABs are more effective than
CC murine MAB 1C11 since they have an increased compatibility in
CC humans. The heavy and light chain V-regions are joined by
CC manipulating their respective joining (J) regions, to generate
CC restriction enzyme recognition sites. The chimeric MABs can be
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV.
CC See also AAQ12056-60 and AAQ12062-63.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 127 AA;
Query Match 89.3%; Score 590; DB 12; Length 127;
Best Local Similarity 89.7%; Pred. No. 3.7e-38;
Matches 113; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Qy 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
Search completed: October 22, 2003, 22:16:35
Job time : 59.2462 secs

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX WPI; 1991-178106/24.
DR N-PSDB; AAQ12017.
XX New chimeric mouse human antibodies - used in treatment, diagnosis
PT and prophylaxis of HIV infections.
XX Disclosure; Fig 13; 108pp; English.
XX The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 126 AA;
Query Match 89.3%; Score 590; DB 12; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.7e-38;
Matches 113; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Qy 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
RESULT 15
AAR12359
ID AAR12359 standard; Protein; 127 AA.
XX AC AAR12359;
XX 25-MAR-2003 (updated)
DT 15-AUG-1991 (first entry)
XX DE Light (kappa) chain variable region of murine 1C11 immunoglobulin.
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX Mus musculus.
XX W09107493-A.
XX 30-MAY-1991.
XX 13-NOV-1990; 90WO-US06615.
XX 13-NOV-1989; 89US-0433730.
XX (XOMA ) XOMA CORP.
XX (GEC ) GREEN CROSS CORP.
XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX WPI; 1991-178105/24.
DR N-PSDB; AAQ12061.
XX New chimeric mouse-human antibodies - used to detect, kill and
PT remove HIV-1 antigen from sample
XX Disclosure; fig 13; 107pp; English.
XX

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| Result No. | Score | Query |        | DB | ID     | Description        |
|------------|-------|-------|--------|----|--------|--------------------|
|            |       | Match | Length |    |        |                    |
| 1          | 632   | 95.6  | 126    | 2  | A34904 | Ig kappa chain pre |
| 2          | 627   | 94.9  | 128    | 2  | PH1224 | Ig kappa chain pre |
| 3          | 625   | 94.6  | 128    | 2  | A26406 | Ig kappa chain v r |
| 4          | 607   | 91.8  | 122    | 2  | A29380 | Ig kappa chain pre |
| 5          | 584   | 88.4  | 115    | 2  | A53276 | Ig kappa chain v r |
| 6          | 579   | 87.6  | 115    | 2  | JL0080 | Ig kappa chain pre |
| 7          | 543   | 82.1  | 108    | 2  | S69903 | Ig kappa chain (cl |
| 8          | 538   | 81.4  | 108    | 2  | S69900 | Ig kappa chain (cl |
| 9          | 530   | 80.2  | 108    | 1  | KVMSAR | Ig kappa chain v r |
| 10         | 529   | 80.0  | 107    | 2  | B28044 | Ig kappa chain v r |
| 11         | 529   | 80.0  | 107    | 2  | A28044 | Ig kappa chain v r |
| 12         | 527   | 79.7  | 108    | 2  | S19970 | Ig kappa chain v r |
| 13         | 527   | 79.7  | 108    | 2  | S69902 | Ig kappa chain (cl |
| 14         | 524   | 79.3  | 109    | 2  | PH0888 | Ig kappa chain v r |
| 15         | 523.5 | 79.2  | 108    | 2  | S38862 | Ig kappa chain v r |
| 16         | 520.5 | 78.7  | 107    | 2  | S69901 | Ig kappa chain (cl |
| 17         | 516.5 | 78.1  | 107    | 2  | S69906 | Ig kappa chain (cl |
| 18         | 516   | 78.1  | 107    | 2  | S32188 | Ig kappa chain v r |
| 19         | 513   | 77.6  | 108    | 2  | B28405 | Ig kappa chain v r |
| 20         | 512   | 77.5  | 108    | 2  | C26405 | Ig kappa chain v r |
| 21         | 512   | 77.5  | 108    | 2  | PL0282 | Ig kappa chain v r |
| 22         | 511   | 77.3  | 108    | 2  | S11124 | Ig kappa chain v r |
| 23         | 507   | 76.7  | 107    | 2  | D48677 | Ig kappa chain v-J |
| 24         | 505   | 76.4  | 107    | 2  | B49026 | Ig kappa chain v r |
| 25         | 504   | 76.2  | 105    | 2  | PH0087 | Ig kappa chain v r |
| 26         | 485   | 73.4  | 108    | 2  | B30551 | Ig kappa chain v r |
| 27         | 485   | 73.4  | 111    | 2  | A38740 | Ig kappa chain v r |
| 28         | 480   | 72.6  | 107    | 2  | D48677 | Ig kappa chain v-J |
| 29         | 480   | 72.6  | 107    | 2  | B48677 | Ig kappa chain v-J |







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Query Match      80.0%; Score 529; DB 2; Length 107;
Best Local Similarity 95.3%; Pred. No. 1.9e-39;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRVAISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

RESULT 11
A28044
Ig kappa chain V region (22B5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
C:Accession: A28044
R:Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
A:Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
A:Reference number: A94179; MUID:87317629; PMID:3114744
A:Accession: A28044
A:Molecule type: mRNA
A:Residues: 1-107 <ME>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.0%; Score 529; DB 2; Length 107;
Best Local Similarity 95.3%; Pred. No. 1.9e-39;
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

RESULT 12
S19970
Ig kappa chain V region (M-T151) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19970
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19970
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <WEI>
A:Cross-references: EMBL:X65095; NID:g52286; PID:CAA46223.1; PID:g52287
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      79.7%; Score 527; DB 2; Length 108;
Best Local Similarity 93.4%; Pred. No. 2.9e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

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Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

RESULT 13
S69902
Ig kappa chain (clone KL2.28) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69902
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69902
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55043; NID:g511027; PID:CAA38883.1; PID:g511028
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      79.7%; Score 527; DB 2; Length 108;
Best Local Similarity 94.3%; Pred. No. 2.9e-39;
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

RESULT 14
PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0888
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann,
J. Exp. Med. 175, 217-225, 1992
A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocyte
A:Reference number: PH0885; MUID:92113462; PMID:1346155
A:Accession: PH0888
A:Molecule type: mRNA
A:Residues: 1-109 <SHA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      79.3%; Score 524; DB 2; Length 109;
Best Local Similarity 93.4%; Pred. No. 5.4e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPTFTGGGTKLEI 106

RESULT 15
S38862
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S38862
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TMV-specific monoclonal antibodies.

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A;Reference number: S37200  
A;Accession: S38862  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-108 <FIS>  
A;Cross-references: EMBL:X75854; NID:9429109; PID:9429110  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 523.5; DB 2; Length 108;  
Best Local Similarity 93.5%; Pred. No. 5.9e-39;  
Matches 100; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

|    |    |   |     |
|----|----|---|-----|
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| Db | 1  | DVQMTQTSSLSAASLGRVTISCRASQDISSYLNWYQOKPDGTIVKLLIYYTSLRLHSGVPS | 60  |
| Qy | 81 | RFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPWTFGGGTKLEI                  | 126 |
| Db | 61 | RFGSGSGTDYSLTISNLEQEDATYFCQGNLTLPWTFGGGTKLEI                  | 107 |

Search completed: October 22, 2003, 22:18:05  
Job time : 25.053 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:20 ; Search time 12.9886 Seconds  
(without alignments)  
459.817 Million cell updates/sec

Title: US-09-114-285A-29

Perfect score: 661

Sequence: 1 MVSSAQLGLLLCFCQTRC.....COQNTLPYTFGGTKLEIN 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match Length | ID           | Description        |
|------------|-------|---------|--------------|--------------|--------------------|
| 1          | 530   | 80.2    | 108          | 1 KV5K_MOUSE | P01644 mus musculu |
| 2          | 528   | 79.9    | 108          | 1 KV5L_MOUSE | P01645 mus musculu |
| 3          | 525   | 79.4    | 108          | 1 KV5N_MOUSE | P01647 mus musculu |
| 4          | 516   | 78.1    | 108          | 1 KV5M_MOUSE | P01646 mus musculu |
| 5          | 513   | 77.6    | 108          | 1 KV5O_MOUSE | P01648 mus musculu |
| 6          | 499   | 75.5    | 108          | 1 KV5U_MOUSE | P04946 mus musculu |
| 7          | 473   | 71.6    | 108          | 1 KV5J_MOUSE | P01643 mus musculu |
| 8          | 451   | 68.2    | 130          | 1 KV5G_MOUSE | P01639 mus musculu |
| 9          | 431   | 65.2    | 129          | 1 KV1W_HUMAN | P04431 homo sapien |
| 10         | 416   | 62.9    | 128          | 1 KV5E_MOUSE | P01637 mus musculu |
| 11         | 412   | 62.3    | 117          | 1 KV1I_HUMAN | P01601 homo sapien |
| 12         | 406   | 61.4    | 108          | 1 KV5P_MOUSE | P01649 mus musculu |
| 13         | 400   | 60.5    | 108          | 1 KV1O_HUMAN | P01607 homo sapien |
| 14         | 400   | 60.5    | 129          | 1 KV1X_HUMAN | P04432 homo sapien |
| 15         | 395   | 59.8    | 108          | 1 KV1Y_HUMAN | P01608 homo sapien |
| 16         | 393   | 59.5    | 108          | 1 KV1P_HUMAN | P01608 homo sapien |
| 17         | 387   | 58.5    | 108          | 1 KV1B_HUMAN | P01594 homo sapien |
| 18         | 386   | 58.4    | 108          | 1 KV1A_HUMAN | P01593 homo sapien |
| 19         | 384   | 58.1    | 117          | 1 KV1J_HUMAN | P01602 homo sapien |
| 20         | 379   | 57.3    | 108          | 1 KV1E_HUMAN | P01597 homo sapien |
| 21         | 377   | 57.0    | 108          | 1 KV1S_HUMAN | P01611 homo sapien |
| 22         | 377   | 57.0    | 115          | 1 KV5F_MOUSE | P01638 mus musculu |
| 23         | 376   | 56.9    | 108          | 1 KV1H_HUMAN | P01600 homo sapien |
| 24         | 375   | 56.7    | 108          | 1 KV1N_HUMAN | P01606 homo sapien |
| 25         | 374   | 56.6    | 108          | 1 KV1M_HUMAN | P01605 homo sapien |
| 26         | 368   | 55.7    | 108          | 1 KV1D_HUMAN | P01604 homo sapien |
| 27         | 367.5 | 55.6    | 107          | 1 KV1C_HUMAN | P01596 homo sapien |
| 28         | 365   | 55.2    | 117          | 1 KV5H_MOUSE | P01641 mus musculu |
| 29         | 364   | 55.1    | 108          | 1 KV1Q_HUMAN | P01609 homo sapien |
| 30         | 364   | 55.1    | 108          | 1 KV1V_HUMAN | P04430 homo sapien |
| 31         | 363   | 54.9    | 111          | 1 KV3L_MOUSE | P01664 mus musculu |
| 32         | 362   | 54.8    | 108          | 1 KV1R_HUMAN | P01610 homo sapien |
| 33         | 361   | 54.6    | 108          | 1 KV5S_MOUSE | P01652 mus musculu |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 34 | 361   | 54.6 | 111 | 1 KV3H_MOUSE | P01660 mus musculu |
| 35 | 360   | 54.5 | 131 | 1 KV3I_MOUSE | P01661 mus musculu |
| 36 | 358   | 54.2 | 108 | 1 KV5Q_MOUSE | P01650 mus musculu |
| 37 | 358   | 54.2 | 136 | 1 KV5B_MOUSE | P01634 mus musculu |
| 38 | 356   | 53.9 | 111 | 1 KV3M_MOUSE | P01665 mus musculu |
| 39 | 358   | 53.7 | 111 | 1 KV3O_MOUSE | P01667 mus musculu |
| 40 | 354.5 | 53.6 | 133 | 1 KV4E_HUMAN | P06313 homo sapien |
| 41 | 354   | 53.6 | 108 | 1 KV1C_HUMAN | P01595 homo sapien |
| 42 | 354   | 53.6 | 108 | 1 KV1K_HUMAN | P01603 homo sapien |
| 43 | 354   | 53.6 | 108 | 1 KV5T_MOUSE | P01653 mus musculu |
| 44 | 354   | 53.6 | 111 | 1 KV3R_MOUSE | P01670 mus musculu |
| 45 | 354   | 53.6 | 134 | 1 KV4C_HUMAN | P06314 homo sapien |

ALIGNMENTS

RESULT 1  
KV5K\_MOUSE STANDARD; PRT; 108 AA.  
ID KV5K\_MOUSE  
AC P01644;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-V region HP R16.7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype";  
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR PIR; A01927; KMSAR.  
DR HSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT FRAMEWORK-1.  
FT COMPLEMENTARITY-DETERMINING-1.  
FT FRAMEWORK-2.  
FT COMPLEMENTARITY-DETERMINING-2.  
FT FRAMEWORK-3.  
FT COMPLEMENTARITY-DETERMINING-3.  
FT FRAMEWORK-4.  
FT BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; A554642C63EFF597 CRC64;  
Query Match 80.2%; Score 530; DB 1; Length 108;  
Best Local Similarity 95.3%; Pred. No. 2.6e-46;  
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| Db | 1  | DIQWTTTSSLSASLGRVITISCRASODISSYLNWYQOKPDGTTKLIYYTSRLHSGVPS 60 |
| Qy | 81 | RFGSGSGTGYSLTINNLEQEDATYFCQGNLTPYTFGGTKLEI 126                |
| Db | 61 | RFGSGSGTGYSLTINNLEQEDATYFCQGNLTPYTFGGTKLEI 106                |

RESULT 2

KV5L MOUSE  
ID KV5L MOUSE STANDARD; PRT; 108 AA.  
AC P01645;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-V region HP 93G7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63E5F58E CRC64;  
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Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
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QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 126  
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DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-V region HP 124E1.  
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
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RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63E5F58E CRC64;  
Query Match 79.9%; Score 528; DB 1; Length 108;  
Best Local Similarity 95.3%; Pred. No. 4.2e-46;  
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 80  
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 60  
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 126  
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 106

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
-!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653E5EFA2 CRC64;  
Query Match 79.4%; Score 525; DB 1; Length 108;  
Best Local Similarity 94.3%; Pred. No. 8.3e-46;  
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 80  
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 60  
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 126  
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 106  
RESULT 4  
KV5M MOUSE  
ID KV5M MOUSE STANDARD; PRT; 108 AA.  
AC P01646;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-V region HP 123B6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653E5EFA2 CRC64;  
Query Match 79.4%; Score 525; DB 1; Length 108;  
Best Local Similarity 94.3%; Pred. No. 8.3e-46;  
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 80  
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKPDGTLKLIYYTSRLHSGVPS 60  
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 126  
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLPTPTFGGKTLEI 106

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SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;
Query Match 78.1%; Score 516; DB 1; Length 108;
Best Local Similarity 93.4%; Pred. No. 6.6e-45;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDYATFCQGNLTLPYTFGGGKTLEI 126
Db 61 RFGSGSGTDYSLTINLEQEDYATFCQGYMLPRTFFGGGKTLEI 106

RESULT 5
KV5U MOUSE
ID KV5U MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RC Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 77.6%; Score 513; DB 1; Length 108;
Best Local Similarity 91.5%; Pred. No. 1.3e-44;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDYATFCQGNLTLPYTFGGGKTLEI 126
Db 61 RFGSGSGTDYSLTINLEQEDISTYFCQGNALPRTFFGGGKTLEI 106

RESULT 6
KV5U MOUSE
ID KV5U MOUSE STANDARD; PRT; 108 AA.
AC P04946;
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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC
CC EMBL; K00745; AAA38690.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 75.5%; Score 499; DB 1; Length 108;
Best Local Similarity 89.6%; Pred. No. 3.3e-43;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTITCSASQDISYLNWYQKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDYATFCQGNLTLPYTFGGGKTLEI 126
Db 61 RFGSGSGTDYSLTITNLOQEDATYACQGNLTLPYTFGGGKTLEI 106

RESULT 7
KV5J MOUSE
ID KV5J MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
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RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01926; KVM573.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT CHAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 FRAMEWORK-3.
FT DOMAIN 57 88 FRAMEWORK-4.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 71.6%; Score 473; DB 1; Length 108;
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISSLYNMYQQKPDGTIKLLIYTSRLHSGVPS 80
DB 1 DIQMTQTSSLSASLGDRVTISCRASQSIQGNVLYWYQQKPDGTIKLLIYTSRLHSGVPS 60

QY 81 RFSGSGSGDYSLTNLEQEDIAIYFCQGNLTLPYTFGGGPKLEI 126
DB 61 RFSGSGSGDYSLTNLEQEDIAIYFCQGNLTLPYTFGGGPKLEI 106

RESULT 8
KV5G_MOUSE
ID KV5G_MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.B., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation.";
RL Nature 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Burstein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains.";
RL Science 155:465-467(1967).
CC -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE

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CC SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A93211; KVM5M4.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Bence-Jones protein.
FT SIGNAL 1 22
FT CHAIN 23 130 IG KAPPA CHAIN V-V REGION MOPC 41.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT VARIANT 1 12 MISSING (IN 25% OF THE MOLECULES).
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; 5EFE0FE71D5F1BEC CRC64;

Query Match 68.2%; Score 451; DB 1; Length 130;
Best Local Similarity 70.6%; Pred. No. 2.6e-38;
Matches 89; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSLYNMYQQK 60
DB 3 MRPAQIFGFLLLFQGTCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLANWLQOEP 62

QY 61 DGTIKLIYTSRLHSGVPSRFSGSGSGDYSLTNLEQEDIAIYFCQGNLTLPYTFGG 120
DB 63 DGTIKLIYATSSLSLDSGVKPRFSGRSRSGDYSLTSSLESSEDFDYIYCLQYASSPWTFG 122

QY 121 GTKLEI 126
DB 123 GTKLEI 128

RESULT 9
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSSP; P01607; IREI.

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DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding activity; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 65.2%; Score 431; DB 1; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.6e-36;
Matches 86; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 5 AQLGLLLLCFOGTRCDIOMTQTTSSLSASLGDVRTISCRASODISSYLNWYQKPGDTI 64
DB 7 AQLGLLLLMURGARDCIOMTQSPSSLSASVGDVRTITCRASQISNLYLNWYQKPKAP 66
QY 65 KLIYTSRLHSGVPSRFGSGSGTGYSLTINNLEQDIATYFCQGNLTLPYTFGGTKL 124
DB 67 KLIYASSLSQSGVTSRFGSGSGTDTLTISLQPEDSATYTCQSYSTLTFGGQTRL 126
QY 125 EI 126
DB 127 EI 128

RESULT 10
KVSE_MOUSE
ID KVSE_MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
RL Nature 287:603-607(1980).
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CC -----
CC EMBL; V00772; CAA24150.1; -.
DR F01920; KVMST1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Query Match 62.9%; Score 416; DB 1; Length 128;
Best Local Similarity 63.5%; Pred. No. 8.1e-35;
Matches 80; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

QY 1 MVSSAQLGLLLCFOGTRCDIOMTQTTSSLSASLGDVRTISCRASODISSYLNWYQKPK 60
DB 1 MPTPAQLGLLLLMWFFPGIKCDIKMTQSPSSMYASLGVRVITISCRASODINSYLTWFOQKP 60
QY 61 DGTIKLIYTSRLHSGVPSRFGSGSGTGYSLTINNLEQDIATYFCQGNLTLPYTFGG 120
DB 61 GKSPKTLVFRANLVDGVPSRFGSGSGQDPSLTISLSEYEDMGIIYCYQDYDFPLTFGA 120
QY 121 GTKLEI 126
DB 121 GTKLEL 126

RESULT 11
KVII_HUMAN
ID KVII_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL kappa genes and a pseudogene.";
RN Nature 288:730-733(1980).
RP [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";
RN Cell 32:181-189(1983).
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CC -----
CC EMBL; K01322; AAA58930.1; -.
DR EMBL; K01324; AAA58932.1; -.

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DR EMBL; V00558; CAA23824.1; --  
 DR PIR; A01881; KIHU11.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.  
 FT DOMAIN 23 45 FRAMEWORK-1.  
 FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 46 56 FRAMEWORK-2.  
 FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 72 78 FRAMEWORK-3.  
 FT DOMAIN 79 110 FRAMEWORK-4.  
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 45 110 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEFF587 CRC64;  
 Query Match 62.3%; Score 412; DB 1; Length 117;  
 Best Local Similarity 72.1%; Pred. No. 1.8e-34;  
 Matches 80; Conservative 12; Mismatches 19; Indels 0; Gaps 0;  
 QY 5 AQLGLLLLCFGCTRCIDQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTI 64  
 DB 7 AQLGLLLLCFGARCDIQMTQSPSSLSASVGRVTITCRARQGISLWLAWYQKPEKAP 66  
 QY 65 KLLIYVTSRLHSGVSRFSGSGGTDYSLTINLQEDDIATYFCQGNLTP 115  
 DB 67 KSLIYAASSLQSGVSRFSGSGGTDFTLTISLQPEDFATYCCQVNSYP 117  
 RESULT 12  
 KV5P\_MOUSE  
 ID KV5P\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01649;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ig kappa chain V-V regions (Anti-arsonate antibodies).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=77250895; PubMed=70482;  
 RA Capra J.D., Tung A.S., Nisonoff A.;  
 RT "Structural studies on induced antibodies with defined idiotypic specificities. I. The complete amino acid sequence of the light chain variable regions of anti-p-azophenylarsonate antibodies from A/J mice bearing a cross-reactive idiotype.";  
 RL J. Immunol. 119:993-999(1977).  
 CC -!- MISCELLANEOUS: THE MIXTURE SEQUENCED CONTAINED AT LEAST TWO OR THREE DIFFERENT LIGHT CHAINS. PEPTIDES CONTAINING THE FOLLOWING SUBSTITUTIONS WERE ALSO ISOLATED: 3-VAL, 10-ILE, AND 12-LEU; 22-LEU; 36-PHE, 41-GLU, AND 43-ALA; 63-THR AND 68-ARG; 76-SER, 77-SER, 78-VAL, 80-ALA, AND 85-ASP; AND 100-GLN AND 107-ARG.  
 CC PIR; A01928; KVMGAA.  
 DR HSSP; P80362; IWTI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 108 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12056 MW; AE2861E6AAC09DD2 CRC64;  
 Query Match 61.4%; Score 406; DB 1; Length 108;  
 Best Local Similarity 74.5%; Pred. No. 6.7e-34;  
 Matches 79; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
 QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYVTSRLHSGVPS 80  
 DB 1 DIQMTQTPSSLSASLGDRVSISSCRASQDISYLNWYQKPDGTIKLLIYVTSRLTNGVDP 60  
 QY 81 RFSGSGSGTDYSLTINLQEDDIATYFCQGNLTPYTFGGGTKLEI 126  
 DB 61 RFSGSGSGTDFTLTIDPMEEDDTATYFCQSRILPRTFGGTKLEI 106  
 RESULT 13  
 KV10\_HUMAN  
 ID KV10\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01607;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region Rei.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039966; PubMed=1182131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";  
 RL Biochemistry 14:4943-4952(1975).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1REI; 17-FEB-84.  
 DR PDB; 1AR2; 12-NOV-97.  
 DR PDB; 1BWV; 29-DEC-99.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23 FRAMEWORK-1.

```
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 80 82
FT HELIX 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 60.5%; Score 400; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 2.7e-33;
Matches 77; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 21 DIQMTTSSLSASIGDRVTTISCRASQDISSVLNMYQOKPGDTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQSPSSLSASVGDRTVITCQASQDIKYLWYQOTPGKAPKLLIYASNLOQGVPS 60

Qy 81 RFGSGSGCTDYSLTINNLEQEDATYFCQOQNTLPYTFGGGTKLEI 126
Db 61 RFGSGSGCTDYTFITSSLPQEDATYFCQYQSLPYTFGGGTKLQI 106

RESULT 14
KVIX HUMAN
ID KVIX HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X00866; CAA25478.1; ALT TERM.
DR PIR; A01884; KIHU01.
DR HSSP; P80362; 1WTL.

DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match 60.5%; Score 400; DB 1; Length 129;
Best Local Similarity 62.8%; Pred. No. 3.3e-33;
Matches 76; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 5 AQLGLLLLCFOGTRCDIQMTTSSLSASIGDRVTTISCRASQDISSVLNMYQOKPGDTI 64
Db 7 AQLGLLLLMRLVRCDIQMTQSPSSLSASVGDRTVITCRAGHNTITFLSYQOKPGKAP 66

Qy 65 KLLIYTSRLHSGVPSRFGSGSGCTDYSLTINNLEQEDATYFCQOQNTLPYTFGGGTKL 124
Db 67 TLLIYVSNLQGVPSRFGSGSGAEFTLITSSLPQEDATYFCQYQYVNFSTFGGGTKV 126
Qy 125 E 125
Db 127 D 127

RESULT 15
KVIX HUMAN
ID KVIX HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RL light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981)
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
```

Search completed: October 22, 2003, 22:17:09  
Job time : 13.9886 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:13:15 ; Search time 58.2083 Seconds  
(without alignments)  
563.024 Million cell updates/sec

Title: US-09-114-285A-29  
Perfect score: 661  
Sequence: 1 MVSSAQLGLLLLCFQGTCTC.....COQGNLPYTFGGTKLEIN 127

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 613   | 92.7        | 234    | 11 | Q91WF8 mus musculus |
| 2          | 574   | 86.8        | 234    | 11 | Q8R062 mus musculus |
| 3          | 534   | 80.8        | 233    | 11 | Q91WS9 mus musculus |
| 4          | 441   | 66.7        | 127    | 11 | Q925S9 mus musculus |
| 5          | 430   | 65.1        | 107    | 11 | Q9JL84 mus musculus |
| 6          | 392.5 | 59.4        | 107    | 4  | Q96SA9 mus musculus |
| 7          | 390   | 59.0        | 108    | 4  | Q9UL77 homo sapien  |
| 8          | 389   | 58.9        | 234    | 11 | Q8VCP0 mus musculus |
| 9          | 388   | 58.7        | 108    | 4  | Q9UL70 homo sapien  |
| 10         | 370.5 | 56.1        | 107    | 4  | Q9UL81 homo sapien  |
| 11         | 367   | 55.5        | 214    | 11 | Q9LIA5 mus musculus |
| 12         | 363   | 54.9        | 108    | 4  | Q9UL79 mus musculus |
| 13         | 363   | 54.9        | 111    | 11 | Q920E9 mus musculus |
| 14         | 351   | 53.1        | 108    | 11 | Q8VJ70 mus musculus |
| 15         | 348   | 52.6        | 116    | 4  | Q96PF6 homo sapien  |
| 16         | 347   | 52.5        | 234    | 4  | Q8NEK1 homo sapien  |

## ALIGNMENTS

## RESULT 1

| ID   | Q91WF8  | PRELIMINARY;  | PRT; | 234 AA. |
|--|---|---|------|---------|
| AC   | Q91WF8;   |   |      |         |
| DT   | 01-DEC-2001 (T-EMBLrel. 19, Created)                      |   |      |         |
| DT   | 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)         |   |      |         |
| DT   | 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)       |   |      |         |
| DE   | Hypothetical 25.9 kDa protein.                            |   |      |         |
| OS   | Mus musculus (Mouse).                                     |   |      |         |
| OC   | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;   |   |      |         |
| OC   | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. |   |      |         |
| OX   | NCBI_TaxID=10090;   |   |      |         |
| RN   | [1]   |   |      |         |
| RP   | SEQUENCE FROM N.A.  |   |      |         |
| RC   | TISSUE=Colon;   |   |      |         |
| RA   | Strausberg R.;  |   |      |         |
| RL   | Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.   |   |      |         |
| DR   | EMBL; BC015292; AAH15292.1; -                             |   |      |         |
| DR   | InterPro; IPR003006; IG_MHC.                              |   |      |         |
| DR   | InterPro; IPR003596; IG_v.                                |   |      |         |
| DR   | InterPro; IPR001865; Ribosomal_S2.                        |   |      |         |
| DR   | Pfam; PF00047; ig; 2.                                     |   |      |         |
| DR   | SMART; SM00406; IGV; 1.                                   |   |      |         |
| DR   | PROSITE; PS00290; IG_MHC; 1.                              |   |      |         |
| DR   | PROSITE; PS00962; RIBOSOMAL_S2_1; 1.                      |   |      |         |
| KW   | Hypothetical protein.                                     |   |      |         |
| SQ   | SEQUENCE 234 AA; B0D0B0E6E7812D2 CRC64;                   |   |      |         |
| Query Match 92.7%; Score 613; DB 11; Length 234;             |   |   |      |         |
| Best Local Similarity 92.1%; Pred. No. 3.5e-56;              |   |   |      |         |
| Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0; |   |   |      |         |
| Qy   | 1   | MVSSAQLGLLLLCFQGTCTCTTTSSLSASLGDRVTISCRASDIDSYLNWYQKP   | 60   |         |
| Db   | 1   | MVSSAQLGLLLLCFQGTCTCTTTSSLSASLGDRVTISCRASDIDSYLNWYQKP   | 60   |         |
| Qy   | 61  | DGTLKLIYYTSRLHSGVPSRFGSGSGTGYSTINLEQEDATYFCQGNLPYTFGG   | 120  |         |
| Db   | 61  | DGTVKLLIYYTSRLYLGVPSPRFGSGSGTGYSTINLEQEDATYFCQGNTPPTFGS | 120  |         |

QY 121 GTKLEI 126  
 Db 121 GTKLEV 126

## RESULT 2

Q91WS9 PRELIMINARY; PRT; 234 AA.  
 AC Q91WS9; 80.8%; Score 574; DB 11; Length 234;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC027418; AAH27418.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 86.8%; Score 574; DB 11; Length 234;

Best Local Similarity 87.3%; Pred. No. 5.8e-54;

Matches 110; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
 Db 1 MVSSAQFLGILLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
 QY 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGG 120  
 Db 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGG 120  
 QY 121 GTKLEI 126  
 Db 121 GTKLEI 126

## RESULT 3

Q91WS9 PRELIMINARY; PRT; 233 AA.  
 AC Q91WS9; 86.8%; Score 574; DB 11; Length 234;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 25.8 kDa protein (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013496; AAH13496.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2.

DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 80.8%; Score 534; DB 11; Length 233;

Best Local Similarity 87.1%; Pred. No. 1.2e-49;

Matches 101; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 11 LLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKPDTIKLLIYY 70  
 Db 10 LLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKPDTIKLLIYY 69  
 QY 71 TSLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGGGTKLEI 126  
 Db 70 TSLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGGGTKLEI 125

## RESULT 4

Q925S9 PRELIMINARY; PRT; 127 AA.  
 AC Q925S9; 87.1%; Score 441; DB 11; Length 127;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Immunoglobulin light chain (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Tripathi P.K.; Qin H.; Bhattacharya-Chatterjee M.; Ceriani R.L.;  
 RA Foon K.A.; Chatterjee S.K.;  
 RT "Construction and characterization of a chimeric fusion protein  
 RT consisting of an anti-idiotypic antibody mimicking a breast cancer-  
 RT associated antigen and the cytokine GM-CSF."  
 RL Hybridoma 18:193-202 (1999).  
 DR EMBL; AF124721; AAK55120.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 FT NON\_TER 127  
 SQ SEQUENCE 127 AA; 13794 MW; 13F61BE8BB981FA5 CRC64;

Query Match 66.7%; Score 441; DB 11; Length 127;

Best Local Similarity 69.8%; Pred. No. 6.4e-40;

Matches 88; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
 Db 1 MRAPAQILGFLLLPFGTCDIQMTQSPSSLSASLGDRVSLTCSRASODIGINHLWQOEP 60  
 QY 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGG 120  
 Db 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDIAFYFCQOQNTLPTFTGG 120  
 QY 121 GTKLEI 126  
 Db 121 GTKLEI 126

## RESULT 5

Q9JL84 PRELIMINARY; PRT; 107 AA.  
 ID Q9JL84  
 AC Q9JL84;

```
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206022; AAF69320.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9BL253ACAL1ESD CRC64;

Query Match 65.1%; Score 430; DB 11; Length 107;
Best Local Similarity 78.3%; Pred. No. 7.9e-39;
Matches 83; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 126
Db 61 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 106

RESULT 6
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031 (1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 107
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SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 59.4%; Score 392.5; DB 4; Length 107;
Best Local Similarity 74.8%; Pred. No. 9.1e-35;
Matches 80; Conservative 11; Mismatches 13; Indels 3; Gaps 2;

Qy 21 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 126
Db 61 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 105

RESULT 7
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 59.0%; Score 390; DB 4; Length 108;
Best Local Similarity 71.7%; Pred. No. 1.7e-34;
Matches 76; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQTTSSLSASLGDRTVISCASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 60

Qy 81 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 126
Db 61 RFSGSGSDTSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 106

RESULT 8
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
[1]
RN  SEQUENCE FROM N.A.
RC  TISSUE-Colon;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC019474; AAH19474.1; -.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; ig; 2.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match      58.9%; Score 389; DB 11; Length 234;
Best Local Similarity 61.2%; Pred.No. 6.1e-34;
Matches 74; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY  6 QFLGLLLCFQGTCTDIQWTTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIK 65
DB  6 QVLGILLCLTGARDIQLTQSPASLSASVGETVITCRASENIYSYLAWYQOKGKSPQ 65

QY  66 LLIIYTSRLHSGVPRFSGSGGTGYSLTINNLEQEDIATYFCQGNLTLPYTFGGGKLE 125
DB  66 LLIVYNAKTADGVPRFSGSGGTQFSLKINSLOPEDFGSYCQHHSGIPPTFGSGTKLE 125

QY  126 I 126
DB  126 I 126

RESULT 9
Q9UL70  PRELIMINARY; PRT; 108 AA.
ID  Q9UL70
AC  Q9UL70
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035033; AAD56269.1; -.
DR  HSSP; P01607; IREI.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match      58.7%; Score 388; DB 4; Length 108;
Best Local Similarity 71.7%; Pred. No. 2.8e-34;
Matches 76; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY  21 DIQWTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIKLLIYTSRLHSGVPS 80
DB  1 DIQWTSPPSSLSASVGDRTVITCRASQGISNYLNWYQOKPGKAPNLLIYAASLSQSGVPS 60

QY  81 RFGSGSGTDFTLTINNLEQEDIATYFCQGNLTLPYTFGGGKLEI 126
DB  61 RFGSGSGTDFTLTISGLQAEEDFATYCCQSYS-ALTFGPGTKYDI 105

RESULT 11
Q9RIAS  PRELIMINARY; PRT; 214 AA.
ID  Q9RIAS
AC  Q9RIAS
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Kappa light chain of Mab7 (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Wilde K.G., Yu X., Ekrasmoddullah A.K.M., Misra S.;
RT  "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
   antibody (Mab 7, its light and heavy chains) and construction of a
   single chain antibody (scFv).";
RL  Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF152371; AAD40242.1; -.
DR  HSSP; P01679; 2FEJ.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; IG_MHC.
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Db  61 RFGSGSGTDFTLTISQLQPEDVATYCYCKYNSAPRTFGPGTKLEI 106

RESULT 10
Q9UL81  PRELIMINARY; PRT; 107 AA.
ID  Q9UL81
AC  Q9UL81
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035033; AAD56269.1; -.
DR  HSSP; P01607; IREI.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 107
SQ  SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      56.1%; Score 370.5; DB 4; Length 107;
Best Local Similarity 69.8%; Pred. No. 2.2e-32;
Matches 74; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

QY  21 DIQWTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIKLLIYTSRLHSGVPS 80
DB  1 DIQWTSPPSSLSASVGDRTVITCRASQGISNYLNWYQOKPGKAPNLLIYAASLSQSGVPS 60

QY  81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGGGKLEI 126
DB  61 RFGSGSGTDFTLTISGLQAEEDFATYCCQSYS-ALTFGPGTKYDI 105

RESULT 11
Q9RIAS  PRELIMINARY; PRT; 214 AA.
ID  Q9RIAS
AC  Q9RIAS
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Kappa light chain of Mab7 (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Wilde K.G., Yu X., Ekrasmoddullah A.K.M., Misra S.;
RT  "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
   antibody (Mab 7, its light and heavy chains) and construction of a
   single chain antibody (scFv).";
RL  Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF152371; AAD40242.1; -.
DR  HSSP; P01679; 2FEJ.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; IG_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.5%; Score 367; DB 11; Length 214;
Best Local Similarity 66.0%; Pred. No. 1.3e-31;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFOQPKGPKTKLIYRANRLVDCGVPS 60

Qy 81 RFGSGSGTGYSLTNINLEQEDDIATYFCQGNLTLPYTFGGGTKEI 126
Db 61 RFGSGSGQDYSLTISSEYEDMGIIYCLQYDEFPFTFGSGTKLEI 106

RESULT 12
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 54.9%; Score 363; DB 4; Length 108;
Best Local Similarity 69.8%; Pred. No. 1.4e-31;
Matches 74; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIVMTQSPSLASGDRVTISCRMSQGISYSLAWYQKPKAPPELLIYAASTLQSGVPS 60

Qy 81 RFGSGSGTGYSLTNINLEQEDDIATYFCQGNLTLPYTFGGGTKEI 126
Db 61 RFGSGSGTDFTLTISCLQSEDFATYCYQYSPFPPTFGQGTKEI 106

RESULT 13
Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.5%; Score 367; DB 11; Length 214;
Best Local Similarity 66.0%; Pred. No. 1.3e-31;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFOQPKGPKTKLIYRANRLVDCGVPS 60

Qy 81 RFGSGSGTGYSLTNINLEQEDDIATYFCQGNLTLPYTFGGGTKEI 126
Db 61 RFGSGSGQDYSLTISSEYEDMGIIYCLQYDEFPFTFGSGTKLEI 106

RESULT 14
Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VKI9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233 (1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 53.1%; Score 351; DB 11; Length 108;
Best Local Similarity 60.4%; Pred. No. 2.8e-30;
Matches 64; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
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QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80  
Db 1 DIWMTQSFMTSVGDRVSVTCKASQNVGTWVWYQKPGQSPKALIYSASYPISGVPH 60  
QY 81 RFSGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYFGGKLEI 126  
Db 61 RTGGSGGTDFTLTISNVQSEDLAEYFCQYNSYPYFGGKLEI 106

RESULT 15

Q96PF6 PRELIMINARY; PRT; 116 AA.  
AC Q96PF6;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE Kappa 1 light chain variable region (Fragment).  
GN SDNK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis:  
RT contributions of Ig V(L) germ line gene use and clonal plasma cell  
RT burden."  
RL Blood 98:714-720(2001).  
DR EMBL; AF361758; AAK51465.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 116  
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 52.6%; Score 348; DB 4; Length 116;  
Best Local Similarity 62.9%; Pred. No. 6.6e-30;  
Matches 66; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80  
Db 1 DIWMTQSFMTSVGDRVSVTCKASQNVGTWVWYQKPGQSPKALIYSASYPISGVPH 60  
QY 81 RFSGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYFGGKLEI 125  
Db 61 RTGGSGGTDFTLTISNVQSEDLAEYFCQYNSYPYFGGKLEI 105

Search completed: October 22, 2003, 22:20:15  
Job time : 60.2083 secs



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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-29

Query Match      100.0%; Score 661; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120

Qy 121 GTKLEIN 127
Db 121 GTKLEIN 127

RESULT 2
US-08-436-717-29
; Sequence 29, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-29

Query Match      100.0%; Score 661; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120

Qy 121 GTKLEIN 127
Db 121 GTKLEIN 127

RESULT 3
US-08-236-520-2
; Sequence 2, Application US/08236520
; Patent No. 5591629
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,520
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 27,227
; REFERENCE/DOCKET NUMBER: MMV92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-520-2

Query Match      96.5%; Score 638; DB 1; Length 131;
Best Local Similarity 96.0%; Pred. No. 9.5e-59;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDDIATYFCQGNLTLPYTFGG 120
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Qy 121 GTKLEI 126  
|  
Db 121 GTKLEI 126

## RESULT 4

PCT-US95-05262-2  
; Sequence 2, Application PC/TUS9505262  
; GENERAL INFORMATION:  
; APPLICANT: Mayo Foundation for Medical Education Research  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE  
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05262  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/236,520  
; FILING DATE: April 29, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 27,227  
; REFERENCE/DOCKET NUMBER: MMV92-01 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-05262-2

Query Match 96.5%; Score 638; DB 5; Length 131;  
Best Local Similarity 96.0%; Pred. No. 9,5e-59;  
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
|  
Db 1 MVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTGYSLTINNLEQDIATYFCQOGNTLPYTFGG 120  
|  
Db 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTGYSLTINNLEQDIATYFCQOGNTLPYTFGG 120  
Qy 121 GTKLEI 126  
|  
Db 121 GTKLEI 126

## RESULT 5

US-08-649-100-17  
; Sequence 17, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU

; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,100  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-649-100-17  
Query Match 93.9%; Score 621; DB 3; Length 127;  
Best Local Similarity 93.7%; Pred. No. 5.3e-57;  
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
|  
Db 1 MVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60  
Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTGYSLTINNLEQDIATYFCQOGNTLPYTFGG 120  
|  
Db 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTGYSLTINNLEQDIATYFCQOGNTLPYTFGG 120  
Qy 121 GTKLEI 126  
|  
Db 121 GTKLEI 126  
RESULT 6  
US-08-458-516-5  
; Sequence 5, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-328-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-5

Query Match 93.6%; Score 619; DB 1; Length 127;
Best Local Similarity 92.9%; Pred. No. 8.5e-57;
Matches 117; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
Db 1 MVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIAFYCOQGNLTLPYTFGG 120
Db 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIAFYCOQGNLTLPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 7
US-08-137-117D-37
; Sequence 37, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Hayold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-137-117D-37

Query Match 92.6%; Score 612; DB 1; Length 127;
Best Local Similarity 92.1%; Pred. No. 4.5e-56;
Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
Db 1 MVSTPQFLGLLLICFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIAFYCOQGNLTLPYTFGG 120
Db 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTINNLEQEDIAFYCOQGNLTLPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 8
US-08-436-717-37
; Sequence 37, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
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; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-37

Query Match 92.6%; Score 612; DB 2; Length 127;
Best Local Similarity 92.1%; Pred. No. 4.5e-56;
Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MVSTPQFLGLLLICFQGTGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 9
US-08-574-699A-2
; Sequence 2, Application US/08574699A
; Patent No. 5985278
; GENERAL INFORMATION:
; APPLICANT: MITJANS, Francesc
; APPLICANT: PIULATS, Jaume
; APPLICANT: ROSELL, Elisabet
; APPLICANT: ADAN, Jaume
; APPLICANT: GOODMAN, Simon
; APPLICANT: HAHN, Diane
; TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,699A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94120165.9
; FILING DATE: 20-DEC-1994
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; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1743
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-699A-2

Query Match 91.7%; Score 606; DB 2; Length 127;
Best Local Similarity 90.5%; Pred. No. 1.9e-55;
Matches 114; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MVSSAQLGLLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKVEM 126

RESULT 10
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 8437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-1101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-10

Query Match 86.8%; Score 574; DB 4; Length 128;
Best Local Similarity 86.5%; Pred. No. 3.9e-52;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MMSSAQLGLLLLCFQGTGRCDIQMTQTASSLPASLGDRVTISCRASODISSYLNWYQOKP 60
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match      86.8%; Score 574; DB 4; Length 128;
Best Local Similarity 86.5%; Pred. No. 3.9e-52;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MMSAQLGLLLLCFQGTCDIQMTQTASSLPASLGDRVTISCSASODISNYLNWYQKP 60
Qy 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIFVSSNLHSGVPSRFGSGGSDYSLTISNLEPEDIATYFCHQYKSLPWTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 14
US-08-836-561-29
; Sequence 29, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-561-29

Query Match      84.1%; Score 556; DB 3; Length 127;
Best Local Similarity 84.1%; Pred. No. 2.8e-50;
Matches 106; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MMSAQLGLLLLCFQGTCDIQMTQTASSLPASLGDRVTIGCTSEDINYNLWYRKKP 60
Qy 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVELLIYHTSLQSGVPSRFGSGGSDYSLTISDLEQEDIATYFCQOGYTLPTVGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 15
US-09-434-122-29
; Sequence 29, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6538111uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-NO. 6538111-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
; US-09-434-122-29

Query Match      84.1%; Score 556; DB 4; Length 127;
Best Local Similarity 84.1%; Pred. No. 2.8e-50;
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Matches 106; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MUSSAQFLGILLCFQGTCDIQMTQTTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MUSSAQFLGILLCFQGTCDIQMTQTTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRPSGSGGTGYSLTINNLEQEDATYFCQOQNTLPYTFGG 120
Db 61 DGTVELLIYHSRLOSQVPSRPSGSGGTGYSLTINNLEQEDATYFCQOQNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
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Search completed: October 22, 2003, 22:20:49  
Job time : 14.4697 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 22:16:46 ; Search time 23.572 Seconds  
(without alignments)  
902.237 Million cell updates/sec

Title: US-09-114-285A-29

Perfect score: 661

Sequence: 1 MVSSAFLGLLLCFQGR.....CQGNLPTVFGGKLEIN 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
|------------|-------|-------------|--------|-------|------------------|
| 1          | 638   | 96.5        | 131    | 8     | US-08-779-784-21 |
| 2          | 638   | 96.5        | 131    | 12    | US-10-010-729-64 |
| 3          | 626   | 94.7        | 127    | 12    | US-10-268-883-5  |
| 4          | 621   | 93.9        | 127    | 15    | US-10-084-139-2  |
| 5          | 574   | 86.8        | 128    | 9     | US-09-764-304-10 |
| 6          | 574   | 86.8        | 128    | 9     | US-09-764-304-19 |
| 7          | 574   | 86.8        | 128    | 12    | US-10-166-626-10 |
| 8          | 574   | 86.8        | 128    | 12    | US-10-166-626-19 |
| 9          | 574   | 86.8        | 128    | 15    | US-10-265-713-10 |
| 10         | 574   | 86.8        | 128    | 15    | US-10-265-713-19 |
| 11         | 556   | 84.1        | 127    | 15    | US-10-283-349-29 |
| 12         | 534   | 80.8        | 108    | 14    | US-10-140-555-4  |
| 13         | 526   | 79.6        | 107    | 12    | US-10-268-883-6  |
| 14         | 526   | 79.6        | 107    | 15    | US-10-269-010-2  |
| 15         | 524   | 79.3        | 601    | 10    | US-09-480-236-1  |

|    |     |      |     |    |                   |                   |
|----|-----|------|-----|----|-------------------|-------------------|
| 16 | 523 | 79.1 | 107 | 12 | US-10-310-674A-34 | Sequence 34, Appl |
| 17 | 517 | 78.2 | 108 | 15 | US-10-141-908-7   | Sequence 7, Appl  |
| 18 | 512 | 77.5 | 214 | 9  | US-09-754-998-1   | Sequence 1, Appl  |
| 19 | 512 | 77.5 | 274 | 9  | US-09-813-659-30  | Sequence 30, Appl |
| 20 | 512 | 77.5 | 302 | 9  | US-09-813-659-18  | Sequence 18, Appl |
| 21 | 512 | 77.5 | 302 | 9  | US-09-813-659-32  | Sequence 32, Appl |
| 22 | 512 | 77.5 | 504 | 15 | US-10-207-655-348 | Sequence 348, App |
| 23 | 508 | 76.9 | 127 | 15 | US-10-283-349-71  | Sequence 71, Appl |
| 24 | 506 | 76.6 | 127 | 15 | US-10-283-349-103 | Sequence 103, App |
| 25 | 505 | 76.4 | 107 | 15 | US-10-011-931-4   | Sequence 4, Appl  |
| 26 | 496 | 75.0 | 127 | 15 | US-10-283-349-98  | Sequence 98, Appl |
| 27 | 493 | 74.6 | 127 | 15 | US-10-283-349-88  | Sequence 88, Appl |
| 28 | 492 | 74.4 | 127 | 15 | US-10-283-349-92  | Sequence 92, Appl |
| 29 | 487 | 73.7 | 108 | 9  | US-09-056-160B-10 | Sequence 10, Appl |
| 30 | 486 | 73.5 | 108 | 12 | US-10-234-671-10  | Sequence 10, Appl |
| 31 | 486 | 73.5 | 109 | 11 | US-10-197-080-4   | Sequence 4, Appl  |
| 32 | 478 | 72.3 | 109 | 11 | US-09-929-665-21  | Sequence 21, Appl |
| 33 | 478 | 72.3 | 109 | 11 | US-09-929-546-21  | Sequence 21, Appl |
| 34 | 463 | 70.0 | 127 | 15 | US-10-084-139-6   | Sequence 6, Appl  |
| 35 | 459 | 69.4 | 107 | 11 | US-09-892-613C-10 | Sequence 10, Appl |
| 36 | 456 | 69.0 | 108 | 9  | US-09-905-243-73  | Sequence 73, Appl |
| 37 | 456 | 69.0 | 130 | 8  | US-08-779-784-35  | Sequence 35, Appl |
| 38 | 456 | 69.0 | 130 | 12 | US-10-010-729-71  | Sequence 71, Appl |
| 39 | 449 | 67.9 | 234 | 9  | US-09-740-002-24  | Sequence 24, Appl |
| 40 | 447 | 67.6 | 105 | 15 | US-10-141-908-31  | Sequence 31, Appl |
| 41 | 447 | 67.6 | 214 | 9  | US-09-940-166A-2  | Sequence 2, Appl  |
| 42 | 447 | 67.6 | 214 | 9  | US-09-811-384-11  | Sequence 11, Appl |
| 43 | 447 | 67.6 | 236 | 10 | US-09-859-053-30  | Sequence 30, Appl |
| 44 | 447 | 67.6 | 237 | 9  | US-09-940-166A-6  | Sequence 6, Appl  |
| 45 | 447 | 67.6 | 237 | 15 | US-10-227-694-1   | Sequence 1, Appl  |

#### ALIGNMENTS

#### RESULT 1

US-08-779-784-21  
; Sequence 21, Application US/08779784  
; Publication No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-784-21

Query Match          96.5%; Score 638; DB 8; Length 131;
Best Local Similarity 96.0%; Pred. No. 1.5e-51;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTLPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 2
US-10-010-729-64
; Sequence 64, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-64

Query Match          96.5%; Score 638; DB 12; Length 131;
Best Local Similarity 96.0%; Pred. No. 1.5e-51;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTLPYTFGG 120
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QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 3
US-10-268-883-5
; Sequence 5, Application US/10268883
; Publication No. US20030138862A1
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Green, Jennifer Macphate
; TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
; FILE REFERENCE: 05882.0062.NPUS01
; CURRENT APPLICATION NUMBER: US/10/268,883
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: USN 60/329,178
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: USN 60/331,965
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mouse
US-10-268-883-5

Query Match          94.7%; Score 626; DB 12; Length 127;
Best Local Similarity 93.7%; Pred. No. 1.9e-50;
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRSODISKYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIAFYCQOQNTVPYTFGG 120
QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 4
US-10-084-139-2
; Sequence 2, Application US/10084139
; Publication No. US20030109416A1
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: YATOMI, Takehiro
; APPLICANT: SUDA, Takashi
; TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
; FILE REFERENCE: 1110-0307P
; CURRENT APPLICATION NUMBER: US/10/084,139
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-084-139-2

Query Match          93.9%; Score 621; DB 15; Length 127;
Best Local Similarity 93.7%; Pred. No. 5.4e-50;
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Db 1 MMSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
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RESULT 6  
US-09-764-304-19  
; Sequence 19, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, NAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA

```

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
;
US-09-764-304-19

Query Match      86.8%; Score 574; DB 9; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY      1 MVSSAQFLGLLLCFGQTRCDIQMTQTTSLSASLGRVITISCRASODISSYLNWYQOKP 60
DB      1 MWSSAQFLGLLLCFGQTRCDIQMTQTASSLPASLGRVITISCRASODISNYLNWYQOKP 60
QY      61 DGTIKLLIYYTSELHSGVSPRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
DB      61 DGTVKLLIYYSNLHSGVSPRFGSGSGTDYSLTINNLEPEDATYFCHQYKSLPWTFGG 120
QY      121 GTKLEI 126
DB      121 GTKLEI 126

RESULT 7
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10

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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-10

Query Match      86.8%; Score 574; DB 12; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0

QY    1 MVSSAQFLGLLLLCFQGTRCDIQMTQTSSLSASLGRVTTISCRASQDISSYLNWYQQKP 60
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     1 MMSSAQFLGLLLLCFQGTRCDIQMTQTASSLPASLGRVTTISCSASQDISNYLNWYQQKP 60
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    61 DGTIKLLIYTSRLHSGVPSPFSGGGTGYSLTIINNLEQEDIIATYFCQCGNTLPYTFGG 120
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     61 DGTVKLLIFYSNNLHSGVPSRFGGGGTGYSLTISNLEPEDIIATYFCHQYSKLPWTFFG 120
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    121 GTKLEI 126
        |||||
Db     121 GTKLEI 126
        |||||

RESULT 8
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHITHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166.626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-166-626-19

Query Match      86.8%; Score 574; DB 12; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0

QY    1 MVSSAQFLGLLLLCFQGTRCDIQMTQTSSLSASLGRVTTISCRASQDISSYLNWYQQKP 60
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     1 MMSSAQFLGLLLLCFQGTRCDIQMTQTASSLPASLGRVTTISCSASQDISNYLNWYQQKP 60
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    61 DGTIKLLIYTSRLHSGVPSPFSGGGTGYSLTIINNLEQEDIIATYFCQCGNTLPYTFGG 120
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     61 DGTVKLLIFYSNNLHSGVPSRFGGGGTGYSLTISNLEPEDIIATYFCHQYSKLPWTFFG 120
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
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; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-265-713-19

Query Match      86.8%; Score 574; DB 15; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MMSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDTIATYFCQOQNTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDTIATYFCQOQNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 11
US-10-283-349-29
; Sequence 29, Application US/10283349
; Publication No. US20030096977A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, No. US20030096977A1uo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997

; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-283-349-29

Query Match      84.1%; Score 556; DB 15; Length 127;
Best Local Similarity 84.1%; Pred. No. 5.3e-44;
Matches 106; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Db 1 MMSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDTIATYFCQOQNTLPYTFGG 120
Db 61 DGTVELLIYHTSRLQSGVPSRFGSGGSDTYSLTINLEQEDTIATYFCQOQNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 12
US-10-140-555-4
; Sequence 4, Application US/10140555
; Publication No. US20020127227A1
; GENERAL INFORMATION:
; APPLICANT: Julie A. Abrahamson
; APPLICANT: Stephen D. Holmes
; APPLICANT: Jeffrey R. Jackson
; TITLE OF INVENTION: RHAMM Antagonist Antibodies
; FILE REFERENCE: PS0857
; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-140-555-4

Query Match      80.8%; Score 534; DB 14; Length 108;
Best Local Similarity 96.2%; Pred. No. 4.7e-42;
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKPDGTLKLIYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKPDGTLKLIYTSRLHSGVPS 60
Qy 81 RFGSGGSDTYSLTINNLEQEDTIATYFCQOQNTLPYTFGGGTKEI 126
Db 61 RFGSGGSDTYSLTINNLEQEDTIATYFCQOQNTLPYTFGGGTKEI 106
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